

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 240 a 210 c 208 g 191 t 20 others
 ORIGIN

Query Match 43.7%; Score 798; DB 9; Length 869;
 Best Local Similarity 96.3%; Pred. No. 7,1e-128;
 Matches 836; Conservative 20; Mismatches 5; Indels 7; Gaps 4;

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QY 2 GGGGATGTCCTGCTGCTGATTAAGCTTGGCCGCTGTGACAGAGCCGTAACCCGAGA 61
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Db 1 GGGGAGTCTGCTGCTGCTGATTAAGCTTGGCCGCTGTGACAGAGCCGTAACCCGAGA 60

QY 62 GCGGACCGTTCAATGAGTCTGTAAGCTGAGGCACTCCAGAGTGAATGCTACAAACATGA 121
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Db 61 GCGGACCGTTCAATGAGTCTGTAAGCTGAGGCACTCCAGAGTGAATGCTACAAACATGA 120

QY 122 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACTGTTCACACTAGTGTGCAAC 181
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Db 121 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACTGTTCACACTAGTGTGCAAC 180

QY 182 AGGGGACTATTCAATTTTGAATGAATGAAGTGGTACTCCGGGAGATGCCAGATCCG 241
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Db 181 AGGGGACTATTCAATTTTGAATGAATGAAGTGGTACTCCGGGAGATGCCAGATCCG 240

QY 242 CTGTGTAAGGCGCACCAAGATTTGTGACGGGCAAAAGCACTCCAGTCTACAGCTG 301
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Db 241 CTGTGTAAGGCGCACCAAGATTTGTGACGGGCAAAAGCACTCCAGTCTACAGCTG 300

QY 302 TGTGAGGT-GCAATTACACAGAGGCC---TTCAGACTC-AGAACAAGCCCTGTGGTGG 355
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TGTGAGGTGCAATTACACAGAGGACATATCCAGCTCAGAGCCAGTCTGTGGMG 350

QY 356 TAAATGACATTTTCTATATTCGGCTTCCCTGTAGAGCTGAACAAGTAT-TTCAATTG 414
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 TAAATGACATTTTCTATATTCGGCTTCCCTGTAGAGCTGAACAAGTAT-TTCAATTG 414

QY 415 GGGCCCAATATTTCTATATTCGAAATATGAATGAAGTGGCCCTCCAGTCTGTGAATT 474
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 415 GGGCCCAATATTTCTATATTCGAAATATGAATGAAGTGGCCCTCCAGTCTGTGAATT 474

QY 475 TCACCTCACCAGGCTGCTGACACATATGAATATTAATAAAGTGTGTCAAGCCG 534
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 475 TCACCTCACCAGGCTGCTGACACATATGAATATTAATAAAGTGTGTCAAGCCG 534

QY 535 GAAGCTGTGGGATCCGAATATCATCTGCTGTGAAGAAATGAGAGACATGTGAAGTGA 594
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 535 GAAGCTGTGGGATCCGAATATCATCTGCTGTGAAGAAATGAGAGACATGTGAAGTGA 594

QY 595 ACTTCAACAACATCTCCCTGAGGAAACAGATACATGCTCTTATCCAAACAGAGACTATCA 654
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 595 ACTTCAACAACATCTCCCTGAGGAAACAGATACATGCTCTTATCCAAACAGAGACTATCA 654

QY 601 ACTTCAACAACATCTCCCTGAGGAAACAGATACATGCTCTTATCCAAACAGAGACTATCA 660
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QY 655 TCGGATTTTCTCAGTGTGTTGAGCCACACAGAAAGAAACAAAGCGAGCTTCAAGTGTGA 714
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Db 655 TCGGATTTTCTCAGTGTGTTGAGCCACACAGAAAGAAACAAAGCGAGCTTCAAGTGTGA 714

QY 715 TTCAGTACTGGGAGATGAGAGTGTACAGGTGACGTACTCCATATTTTCTACTT 774
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Db 715 TTCAGTACTGGGAGATGAGAGTGTACAGGTGACGTACTCCATATTTTCTACTT 774

QY 775 GTGGGACGACATGATCCGACATTAAGGAAACAGTGTGCTCTGCCCAACAAGGGGTCC 834
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 775 GTGGGACGACATGATCCGACATTAAGGAAACAGTGTGCTCTGCCCAACAAGGGGTCC 834

QY 840 GTGGGACGACATGATCCGACATTAAGGAAACAGTGTGCTCTGCCCAACAAGGGGTCC 840
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Db 840 GTGGGACGACATGATCCGACATTAAGGAAACAGTGTGCTCTGCCCAACAAGGGGTCC 840
  
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QY 835 CTTTCCTCTGTGATACAAACAAGAACAA 862
 Db 841 CTTTCCTCTGTGATACAAACAAGAACAA 868

RESULT 2
 LOCUS BI823321 946 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603041231F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182255 5',
 mRNA sequence.
 ACCESSION BI823321
 VERSION BI823321.1 GI:15934871
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contract: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: LLM11454 row: m column: 08
 High quality sequence stop: 795.
 Location/Qualifiers

FEATURES
 source 1..946
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5182255"
 /clone_1ib="NIH MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

BASE COUNT 240 a 239 c 243 g 224 t
 ORIGIN

Query Match 41.9%; Score 766.2; DB 13; Length 946;
 Best Local Similarity 91.3%; Pred. No. 2,1e-122;
 Matches 910; Conservative 0; Mismatches 33; Indels 54; Gaps 7;

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QY 2 GGGGATGTCCTGCTGCTGATTAAGCTTGGCCGCTGTGACAGAGCCGTAACCCGAGA 61
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Db 1 GGGGATGTCCTGCTGCTGATTAAGCTTGGCCGCTGTGACAGAGCCGTAACCCGAGA 60

QY 62 GCGGACCGTTCAATGAGTCTGTAAGCTGAGGCACTCCAGAGTGAATGCTACAAACATGA 121
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GCGGACCGTTCAATGAGTCTGTAAGCTGAGGCACTCCAGAGTGAATGCTACAAACATGA 120

QY 122 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACTGTTCACACTAGTGTGCAAC 181
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACTGTTCACACTAGTGTGCAAC 180

QY 182 AGGGGACTATTCAATTTTGAATGAATGAAGTGGTACTCCGGGAGATGCCAGATCCG 241
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 AGGGGACTATTCAATTTTGAATGAATGAAGTGGTACTCCGGGAGATGCCAGATCCG 240

QY 242 CTGTGTAAGGCGCACCAAGATTTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTG 301
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QY 1549 CCTATCCCAACATTACAGGAAAGAAACGTTGATGATCCTGAAGCTTACTATGACGCT 1608
Db 177 CCTATCCCMCCAAATTACAGGMAAAACGTTGATGATCCTGAAGCTTACTATGACGCT 118
QY 1609 ACAACAGCCTTGTAGTAATTAACAACTTTATACCAATAAAATTTTCAATATTAACCT 1668
Db 117 ACAACAGCCTTGTAGTAATTAACAACTTTATATAMHWAATAAAATTTTCAATATTAACCT 58
QY 1669 AATGTAGCATTAACTAACGATTGGAACATACATTTCACAACTTCAAAAGCTGTTTTATA 1725
Db 57 AATGTAGCATTAACTAACGATTGGAACCTCAITTCACACCCYCAAAGCTGTTTTATA 1

RESULT 4
LOCUS AV709899 703 bp mRNA linear EST 09-OCT-2000
DEFINITION AV709899 ADC Homo sapiens cDNA clone ADCAB04 5', mRNA sequence.
ACCESSION AV709899
VERSION AV709899.1 GI:10728055
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao
AUTHORS H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
G., Hu, R., Chen, J., Chen, Z., and Han, Z.
Homo sapiens cDNA ADC clones
This clone is available at CHGC in Shanghai.
LOCATION/Qualifiers
1..703
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCAB04"
/clone_lib="ADC"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 186 a 172 c 166 g 177 t 2 others
ORIGIN

Query Match 35.3%; Score 645.4; DB 10; Length 703;
Best Local Similarity 97.5%; Pred. No. 1.4e-101;
Matches 655; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 280 GCAACTTCAGTCTCAGTCTCAGCTGTGAGTGCAATTACACAGAGGCTTCCAGACTCAGA 339
Db 1 GCAACTTCAGTCTCAGTCTCAGCTGTGAGTGCAATTACACAGAGGCTTCCAGACTCAGA 60
QY 340 CCAGACCCCTCTGGTGGTAATGGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACA 399
Db 61 CCAGACCCCTCTGGTGGTAATGGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACA 120
QY 400 CAGTCTATTTCATTTGGGGCCCAATAATTCTTAATGCAAAATGATGAAGATGCGCCCTT 459
Db 121 CAGTCTATTTCATTTGGGGCCCAATAATTCTTAATGCAAAATGATGAAGATGCGCCCTT 180
QY 460 CCATGCTCTGTAATTTTCACCTCACCAGGCTGCTAGACCACACATAATGAATAATAAAAAA 519
Db 181 CCATGCTCTGTAATTTTCACCTCACCAGGCTGCTAGACCACACATAATGAATAATAAAAAA 240

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QY 520 AGTGTGTCAAGCCCGGAAGCCCTGTGGGATCCGAACATCACTGCTTTGTGAAGAAGATGAGG 579
Db 241 AGTGTGTCAAGCCCGGAAGCCCTGTGGGATCCGAACATCACTGCTTTGTGAAGAAGATGAGG 300
QY 580 AGACAGTAGAAGTGAACCTTCAACACACTCCCTCGGAAACAGATACATGGCTCTTATCC 639
Db 301 AGACAGTAGAAGTGAACCTTCAACACACTCCCTCGGAAACAGATACATGGCTCTTATCC 360
QY 640 AACACAGCACTATCATCGGTTTCTCAGGTGTTTTCAGGCTGTTTTCAGCCACAGAGAAACAAACGC 699
Db 361 AACACAGCACTATCATCGGTTTCTCAGGTGTTTTCAGGCTGTTTTCAGCCACAGAGAAACAAACGC 420
QY 700 GAGCTTTCAGTGTGATTCAGTACTGGGGATGATGAAGGTCTACGGTGCAGCTGACTC 759
Db 421 GAGCTTTCAGTGTGATTCAGTACTGGGGATGATGAAGGTCTACGGTGCAGCTGACTC 480
QY 760 CATATTTTCTACTTGTGGCAGCAGCTGCATCCGACATAAAGGAACAGTTGTGCTCTGCC 819
Db 481 CATATTTTCTACTTGTGGCAGCAGCTGCATCCGACATAAAGGAACAGTTGTGCTCTGCC 540
QY 820 CACAAACAGGGTCCCTTTTCCCTCTGGATACAAACAAAGCAAGCGGAGGCTGCTGC 879
Db 541 CACAAACAGGGTCCCTTTTCCCTCTGGATACAAACAAAGCAAGCGGAGGCTGCTGC 600
QY 880 CTCTCCTCTGCTGTCTCTGTGCTGGCCACATGCGGTGCTGTGCGCAGGATCTATCTAA 939
Db 601 CTCTCCTCTGCTGTGCTGTGCTGGCCACATGCGGTGCTGTGCGCAGGATCTATCTAA 660
QY 940 TGTGGAGGCACG 951
Db 661 TGTGGATGCACG 672

RESULT 5
LOCUS BM693867 652 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-DW1-ah-e-i-22-0-UI.r1 UI-E-DW1 Homo sapiens cDNA clone
ACCESSION BM693867
VERSION BM693867.1 GI:19007125
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 652)
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1..652
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-DW1-ah-e-i-22-0-UI"
/clone_lib="UI-E-DW1"
/tissue_type="lens"
/dev_stage="adult"

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FEATURES

source

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 UI-E-DWI is a normalized cDNA library containing the
 following tissue(s): lens. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an Ecor I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CGATTAGCGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."
 BASE COUNT 188 a 167 c 135 g 162 t
 ORIGIN

Query Match 34.9%; Score 638.4; DB 14; Length 652;
 Best Local Similarity 99.7%; Pred. No. 2.3e-100;
 Matches 650; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Qy 961 AGAAGACTTCTTTTACACACACTACTGCCCCCATTAAGGTTCTGTGTTTACC 1020
 Db 1 AGAAGACTTCTTTTACACACACTACTGCCCCCATTAAGGTTCTGTGTTTACC 60
 Qy 1021 CATCTGAATATGTTTCCATCATCACAAATTTGTTACTGAAATTTCTCAAAACCAT 1080
 Db 61 CATCTGAATATGTTTCCATCATCACAAATTTGTTACTTCACTGAATTTCTCAAAACCAT 120
 Qy 1081 GCAGAAGTCAGGTCACTCTTGAAGAGTGCAGAAAAGAAAATAGCAGAGATGGGTCAG 1140
 Db 121 GCAGAAGTCAGGTCACTCTTGAAGAGTGCAGAAAAGAAAATAGCAGAGATGGGTCAG 180
 Qy 1141 TGCAGTGGCTTGCCTCAAAAGAGCGCAGACAAAGTCGTCCTTCTTCTTCCAAATG 1200
 Db 181 TGCAGTGGCTTGCCTCAAAAGAGCGCAGACAAAGTCGTCCTTCTTCTTCCAAATG 240
 Qy 1201 AGCTCAACAGTGTGCGATGTTGACCTGTGGCAAGCAGGCGAGTCCAGTGAAGACT 1260
 Db 241 AGCTCAACAGTGTGCGATGTTGACCTGTGGCAAGCAGGCGAGTCCAGTGAAGACT 300
 Qy 1261 CTCAGACCTTTCCTCCCTTGCCTTTAACTTTTCGAGTATCATTAAGAGCCAGATTC 1320
 Db 301 CTCAGACCTTTCCTCCCTTGCCTTTAACTTTTCGAGTATCATTAAGAGCCAGATTC 360
 Qy 1321 ATCTGCACAAATACGTTGGTCTACTTTAGAGAGATTGATACAAAGACGATTACAATG 1380
 Db 361 ATCTGCACAAATACGTTGGTCTACTTTAGAGAGATTGATACAAAGACGATTACAATG 420
 Qy 1381 CTCTCAGTGTGCCCCCAAGTACCACTTCATGAAGATGCCACTGTTCTGTGCAGAAC 1440
 Db 421 CTCTCAGTGTGCCCCCAAGTACCACTTCATGAAGATGCCACTGTTCTGTGCAGAAC 480
 Qy 1441 TTCTCCATGTCAAGCAGCGGTGTGACGAGGAAAAGATCACAAAGCCTGCCAGATGGCT 1500
 Db 481 TTCTCCATGTCAAGCAGCGGTGTGACGAGGAAAAGATCACAAAGCCTGCCAGATGGCT 540
 Qy 1501 GCTGCTCTTGTAGCCACCCATGAGAAGCAGACCTTAAGGTTCTTATCCACCA 1560
 Db 541 GCTGCTCTTGTAGCCACCCATGAGAAGCAGACCTTAAGGTTCTTATCCACCA 600
 Qy 1561 ATTACAGGG-AAAAACGTTGATGATCTCTGAAGCTTACTATCGACCTTACA 1611
 Db 601 ATTACAGGGAAAAAACGTTGATGATCTCTGAAGCTTACTATCGACCTTACA 652

RESULT 6
 BM670929/c
 LOCUS
 DEFINITION UI-E-DWI-ah-e-i-22-0-UI.s1 UI-E-DWI Homo sapiens cDNA clone
 UI-E-DWI-ah-e-i-22-0-UI 3', mRNA sequence. EST 27-FEB-2002

ACCESSION BM670929
 VERSION BM670929.1
 KEYWORDS GI:18980826
 EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 657)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9585
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Forward
 POLVA=Yes.

FEATURES
 source

Location/Qualifiers
 1..657
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-DWI-ah-e-i-22-0-UI"
 /clone_lib="UI-E-DWI"
 /tissue_type="lens"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 UI-E-DWI is a normalized cDNA library containing the
 following tissue(s): lens. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an Ecor I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CGATTAGCGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI).
 TAG LIB=UI-E-DWI
 TAG TISSUE=human lens
 TAG_SEQ=CGATTAGCGA"

BASE COUNT 167 a 116 c 150 g 224 t

Query Match 34.5%; Score 630.6; DB 13; Length 657;
 Best Local Similarity 98.5%; Pred. No. 5e-99;
 Matches 647; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1161 AAGAAGGCGACGACAAAGTCGTCCTTCTTCCATGACGTCAACAGTGTGCGAT 1220
 Db 657 AAGAAGGCGACGACAAAGTCGTCCTTCTTCCATGACGTCAACAGTGTGCGAT 598
 Qy 1221 GGTACCTGTGGCAAGCAGGCGAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTT 1280
 Db 597 GGTACCTGTGGCAAGCAGGCGAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTT 538
 Qy 1281 GCCTTTAACTTTTCTGAGTGATCTAGAGCCAGATTCATCTGCACAAATACGTGGTG 1340
 Db 537 GCCTTTAACTTTTCTGAGTGATCTAGAGCCAGATTCATCTGCACAAATACGTGGTG 478

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Qy 1341 GTCTACTTTAGAGAGATTGATCAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAG 1400
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Db 477 GTCTACTTTAGAGAGATTGATCAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAG 418
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|
|
Qy 1401 TACCACCTTCATGAAGATGCCACTGCTTCTGTGCGAAGACTTCCATGTCAAGCGAG 1460
|
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|
Db 417 TACCACCTTCATGAAGATGCCACTGCTTCTGTGCGAAGACTTCCATGTCAAGCGAG 358
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Qy 1461 GTGTGACGAGAAAGATGATCAAGAGCTGCGACGATGGCTGCTGCTCTTGTAGCCACC 1520
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Db 357 GTGTGACGAGAAAGATGATCAAGAGCTGCGACGATGGCTGCTGCTCTTGTAGCCACC 298
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Qy 1521 CATGAGAAGCAAGAGACCTTAAAGGCTTCTATPCCACCAATTTACAGGG-AAAAAAGCTG 1579
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Db 297 CATGAGAAGCAAGAGACCTTAAAGGCTTCTATPCCACCAATTTACAGGGAAAAAAGCTG 238
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Qy 1580 TGATGATCTGAAGCTTACTATGCGAGCTTACAAAGAGCTTAGTAATTTAAACATTTTAT 1639
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|
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Db 237 TGATGATCTGAAGCTTACTATGCGAGCTTACAAAGAGCTTAGTAATTTAAACATTTTAT 178
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|
Qy 1640 ACCAATAAAATTTTCAAAATTTACTAACTAACTAGTACATTTAACTACAGATGGAACACTAC 1699
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|
|
Db 177 ACCAATAAAATTTTCAAAATTTACTAACTAACTAGTACATTTAACTACAGATGGAACACTAC 118
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|
Qy 1700 ATTACAACCTTCAAAGCTGTTTATATACATAGAAATCAATTTACAGCTTTTAAATGAAAACTG 1759
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Db 117 ATTACAACCTTCAAAGCTGTTTATATACATAGAAATCAATTTACAGCTTTTAAATGAAAACTG 58
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Qy 1760 TAACCAATTTGATAATGCAACATAAAGCATCTTCCAAAAAAGAAAAAAGAAAAA 1816
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Db 57 TAACCAATTTGATAATGCAACATAAAGCATCTTCCAAAAAAGAAAAAAGAAAAA 1
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RESULT 7
AV727345 676 bp mRNA linear EST 17-OCT-2000
LOCUS AV727345 HTC Homo sapiens cDNA clone HTCACC09 5', mRNA sequence.
DEFINITION AV727345
VERSION AV727345.1 GI:10836766
KEYWORDS EST.
SOURCE human.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCAC09"
/tissue="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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FEATURES
source 190 a 162 c 155 g 169 t
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Query Match 34.4%; Score 628; DB 10; Length 676;
Best Local Similarity 96.9%; Pred. No. 1.4e-98;
Matches 651; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 435 GCAATATGATGAAGATGGCCCTTCCATGCTGTGGAATTTTCCATCCACAGGCTGCCTA 494
|
|
|
Db 1 GCAATATGATGAAGATGGCCCTTCCATGCTGTGGAATTTTCCATCCACAGGCTGCCTA 60
|
|
|
Qy 495 GACCAATAATGAAATATAAAAAAAGTGTGCAAGGCCGGAAGCTCTGGGATCCGAAC 554
|
|
|
Db 61 GACCAATAATGAAATATAAAAAAAGTGTGCAAGGCCGGAAGCTCTGGGATCCGAAC 120
|
|
|
Qy 555 ATCACTGCTTGTAGAAGAAATGAGGAGACAGTAGAAGTGAATTTCAACAACCACTCCCTG 614
|
|
|
Db 121 ATCACTGCTTGTAGAAGAAATGAGGAGACAGTAGAAGTGAATTTCAACAACCACTCCCTG 180
|
|
|
Qy 615 GGAACACATACATGGCTCTTTATCCAAACACAGCACTATCATCGGGTTTTCTCAGGTGTT 674
|
|
|
Db 181 GGAACACATACATGGCTCTTTATCCAAACACAGCACTATCATCGGGTTTTCTCAGGTGTT 240
|
|
|
Qy 675 GAGCCACACCAAGAGAAACAAACGCGAGCTTCAGTGGTGATTTCCAGTCACTGGGGATAGT 734
|
|
|
Db 241 GAGCCACACCAAGAGAAACAAACGCGAGCTTCAGTGGTGATTTCCAGTCACTGGGGATAGT 300
|
|
|
Qy 735 GAAAGTGCTACGGTGACGCTGACTCCATATTTTCTTACTTTGCGAGGCACTGCATCCGA 794
|
|
|
Db 301 GAAAGTGCTACGGTGACGCTGACTCCATATTTTCTTACTTTGCGAGGCACTGCATCCGA 360
|
|
|
Qy 795 CATAAAGGAACAGTTGCTCTGCCCCAACAAACAGCGCTCCCTTCCCTCTGGATTAACAAAC 854
|
|
|
Db 361 CATAAAGGAACAGTTGCTCTGCCCCAACAAACAGCGCTCCCTTCCCTCTGGATTAACAAAC 420
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|
|
Qy 855 AAAAGCAAGCCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 914
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|
|
Db 421 AAAAGCAAGCCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
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|
|
Qy 915 GTGCTGTGGCGAGGATCTATCTAATGTGAGGCAACAAAGGATCAAGAAGACTTTCCTTT 974
|
|
|
Db 481 GTGCTGTGGCGAGGATCTATCTAATGTGAGGCAACAAAGGATCAAGAAGACTTTCCTTT 540
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|
|
Qy 975 TCTACCACCACTACTGCCCCCATTAAGTCTTGTGGTTTACCCTCTGGAATATGT 1034
|
|
|
Db 541 TTTTACCACCACTACTGCTCTCCCATTAAGATCTTGTGGTTTATCCATCTGGAATATGT 600
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|
|
Qy 1035 TTCCATCACACAAATTTTACTTCACTGAATTTCTTCAAAACCAATTGCAGAAGTGAGGTC 1094
|
|
|
Db 601 TTCCATCACACAAATTTTACTTCACTGAATTTCTTCAAAACCAATTGCAGAAGTGAGGTC 659
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Qy 1095 ATCCTTGAAGG 1106
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Db 660 ACTCTTGAAGG 671
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RESULT 8
BE539514
LOCUS BE539514
DEFINITION 601060209F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446667 5',
mRNA sequence.
ACCESSION BE539514
VERSION BE539514.1 GI:9768159
KEYWORDS EST.
SOURCE human.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 641)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
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cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 CDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM8419 row: a column: 04
 High quality sequence stop: 639.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3446667"
 /clone_lib="NIH_MGC_10"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5 kb. Library prepared by Life
 Technologies."

BASE COUNT 206 a 152 c 118 g 165 t

ORIGIN
 Query Match 34.0%; Score 621.6; DB 10; Length 641;
 Best Local Similarity 99.2%; Pred. No. 1.8e-97;
 Matches 635; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1155 ACTCAAAAGAGGCGAGCAGACAAAGTCGCTTCCTTTTCAATGACGTCAACAGTGTG 1214
 DB 1 ACTCAAAAGAGGCGAGCAGACAAAGTCGCTTCCTTTTCAATGACGTCAACAGTGTG 60
 QY 1215 TCGGATGGTACCTGTGGGGAAGCGAGGCGAGTCCAGTGAGAACTCTCAAGACCTTTTC 1274
 DB 61 TCGGATGGTACCTGTGGGGAAGCGAGGCGAGTCCAGTGAGAACTCTCAAGACCTTTTC 120
 QY 1275 CCCCTTGCCCTTAACTTTCTGCACTGATCTAAGAGCCAGATTCATCTGCACAAATAC 1334
 DB 121 CCCCTTGCCCTTAACTTTCTGCACTGATCTAAGAGCCAGATTCATCTGCACAAATAC 180
 QY 1335 GTGGTGGTCTACTTTAGAGAGATTGATACAAAGAGGATTACAACTCTCTCAGTGCTGC 1394
 DB 181 GTGGTGGTCTACTTTAGAGAGATTGATACAAAGAGGATTACAACTCTCTCAGTGCTGC 240
 QY 1395 CCCAAGTACCCTTCATGAAGGATGCCACTGCTTTCTGTGCAAGACTTCTCCATGTCAAG 1454
 DB 241 CCCAAGTACCCTTCATGAAGGATGCCACTGCTTTCTGTGCAAGACTTCTCCATGTCAAG 300
 QY 1455 CAGCAGGTGTACGAGGAAAGATCACAGGCTGCCACGATGGCTGCTCCTTGTAG 1514
 DB 301 CAGCAGGTGTACGAGGAAAGATCACAGGCTGCCACGATGGCTGCTCCTTGTAG 360
 QY 1515 CCCACCCATGAGAAGCAAGAGACCTTAAAGGCTTCTATCCCAACCAATTACAGGGAAAAA 1574
 DB 361 CCCACCCATGAGAAGCAAGAGACCTTAAAGGCTTCTATCCCAACCAATTACAGGGAAAAA 420
 QY 1575 ACGTGTGATGATCTGAAGCTTACTATGAGGCTTCAAAACAGCCTTAGTAATTAACAT 1634
 DB 421 ACGTGTGATGATCTGAAGCTTACTATGAGGCTTCAAAACAGCCTTAGTAATTAACAT 480
 QY 1635 TTTATACCAATAAATTTTCAATATTACTTAATGATGATGATTAACCTAAGATTGNA 1694
 DB 481 TTTATACCAATAAATTTTCAATATTACTTAATGATGATGATTAACCTAAGATTGNA 539
 QY 1695 ACTACATTTACAACTTCAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAA 1754
 DB 540 ACTACATTTACAACTTCAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAA 599
 QY 1755 AACTGTAACCAATTTTGATAATGCAACAATAAAGCATCTTC 1794
 DB 600 AACTGTAACCAATTTTGATAATGCAACAATAAAGCATCTTC 639

RESULT 9

BI458542

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 788)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11702 row: e column: 12

High quality sequence stop: 784.

FEATURES

Location/Qualifiers

1..788

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5278067"

/clone_lib="NIH_MGC_96"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

size-selected for average insert size 2.3 kb and

normalized to 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 196 a 206 c 201 g 184 t 1 others

ORIGIN

Query Match 33.4%; Score 610.4; DB 13; Length 788;

Best Local Similarity 98.9%; Pred. No. 1.4e-95;

Matches 656; Conservative 0; Mismatches 2; Indels 5; Gaps 4;

QY 360 TGGACATTTTCTATATCGGCTTCCCTCTAGAGCTGGAACACAGTCTATTTCATTCGGGCC 419

DB 130 TGGACATTTTCTATATCGGCTTCCCTCTAGAGCTGGAACACAGTCTATTTCATTCGGGCC 189

QY 420 CATATATTTCCCTAAATGCAAAATGAATGAAGATGCCCTTCCATGCTGTGAATTCACC 479

DB 190 CATATATTTCCCTAAATGCAAAATGAATGAAGATGCCCTTCCATGCTGTGAATTCACC 249

QY 480 TCACGAGCTGCTAGACCATATGAATGAATATAAAAAAGTGTCAAGCCGGAAGC 539

DB 250 TCACGAGCTGCTAGACCATATGAATGAATATAAAAAAGTGTCAAGCCGGAAGC 309

QY 540 CTGTGGGATCCGAACATCACTGCTTGTGAAGAGATGAGGAGACAGTAGAGTGAACCTTC 599

DB 310 CTGTGGGATCCGAACATCACTGCTTGTGAAGAGATGAGGAGACAGTAGAGTGAACCTTC 369

QY 600 ACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCCAACACAGCACTATCATCGGG 659

DB 370 ACAACCACTCCCTGGGAAACAGATACATGGCTC--ATCCCAACACAGCACTATCATCGGG 427

QY 660 TTTTCTCAGGTGTTTGAGCCACACAGAGAAACAAACCGGAGCTTTCAGTGGTATTCGA 719

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Db 428 TTTTCTCAGGTGTTTGAGCCACACCAAGAAACAAACGCGAGCTTCAGTGGTGATTCACA 487
QY 720 GTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGCG 779
Db 488 GTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGCG 547
QY 780 AGCGACTGCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAAACAGCGCGTCCCTTTC 839
Db 548 AGCGACTGCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAAACAGCGCGTCCCTTTC 607
QY 840 CTTCTGTAACAAACAAAGCAAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 899
Db 608 CTTCTGTAACAAACAAAGCAAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 667
QY 900 CTGGTGGCCACA-TGGGTGCTGTGGCAGGATCTATCTAATGTGAGCAGCAAGAGAT 958
Db 668 CTGGTGGCACAATTGGGTGCTGTGGCAGGATCTATCTAATGTGAGCAGCAAGAGAT 727
QY 959 CAAGAAGACTTCTTTTCTACCAACACACTACTGCCCCCAATTAAGTTCTTGTGGTTTA 1018
Db 728 C-AGAAGACTTCTTTTCTACCAACACACA-TACTGCCCCCAATTAAGTTCTTGTGGTTTA 785
QY 1019 CCC 1021
Db 786 CCC 788

RESULT 10
LOCUS BG433769/c
DEFINITION 60249774F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4611491 5',
mRNA sequence.
ACCESSION BG433769
VERSION BG433769.1 GI:13340275
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 630)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1358 row: g column: 12
High quality sequence stop: 610.
Location/Qualifiers
1. .630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
170 a 111 c 149 g 200 t
BASE COUNT
ORIGIN

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Query Match 32.7%; Score 598.2; DB.12; Length 630;
Best Local Similarity 97.9%; Pred. No. 1.9e-93;
Matches 506; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1185 TTCCTTCTTTTCAATGAGCTCAACAGTGTGTGCGATGATGCTGTGGCAAGCAGGCGC 1244
Db 626 TCCTTCTTTTCAATGAGCTCAACAGTGTGTGCGATGATGCTGTGGCAAGCAGGCGC 567
QY 1245 AGTCCAGTGTGAAGCTCTCAAGACCTCTTCCCTTGCCTTTAACTTTTCTGCAAGTAT 1304
Db 566 AGTCCAGTGTGAAGCTCTCAAGACCTCTTCCCTTGCCTTTAACTTTTCTGCAAGTAT 507
QY 1305 CTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCTTACTTTAGAGAGATTGATACA 1364
Db 506 CTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCTTACTTTAGAGAGATTGATACA 447
QY 1365 AAAGACGATTCAATGTCTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGGATGCCACT 1424
Db 446 AAAGACGATTCAATGTCTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGGATGCCACT 387
QY 1425 GCTTTCTGTGAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAGATCACA 1484
Db 386 GCTTTCTGTGAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAGATCACA 327
QY 1485 GCCTGCCAGATGGCTGCTCTTGTAGCCACCCATGAGAACCAAGAGACCTTTAAAG 1544
Db 326 GCCTGCCAGATGGCTGCTCTTGTAGCCACCCATGAGAACCAAGAGACCTTTAAAG 267
QY 1545 GCTTCCTATCCCAACAAATTACAGGAAAAAAGCTGTGATGATCTCTGAAAGCTTTATGCA 1604
Db 266 GCTTCCTATCCCAACAAATTACAGGAAAAAAGCTGTGATGATCTCTGAAAGCTTTATGCA 207
QY 1605 GCCTACAAACAGCCTTAGTAATTAACAACTTTATACCAATARAATTTTCAAAATATTACT 1664
Db 206 GCCTACAAACAGCCTTAGTAATTAACAACTTTATACCAATARAATTTTCAAAATATTACT 147
QY 1665 AACTAATGTAGCATTAACTAAGATTGGAATCTCAATTTCAAACTTTCAAGCTGTTTTAT 1724
Db 146 AACTAATGTAGCATTAACTAAGATTGGAATCTCAATTTCAAACTTTCAAGCTGTTTTAT 87
QY 1725 ACATAGAAATCAATTCACAGCTTTTAAATGAAAACCTGTAACTTTGATTAATGCAACAATA 1784
Db 86 ACATAGAAATCAATTCACAGCTTTTAAATGAAAACCTGTAACTTTGATTAATGCAACAATA 27
QY 1785 AAGCATCTTCCAAAAAAA 1803
Db 26 AAGCATCTTCCAGCCAAAACA 8

RESULT 11
LOCUS BI602183
DEFINITION 603244108F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5286745 5',
mRNA sequence.
ACCESSION BI602183
VERSION BI602183.1 GI:15495122
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 842)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

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QY	1024	CTGAATATGTTTTCATCACACAATTTGTTACTTCACTGAAATTTCTTTCAAAACCAATTGCA	1083
Db	1	CTGAATATGTTTTCATCACACAATTTGTTACTTCACTGAAATTTCTTTCAAAACCAATTGCA	60
QY	1084	GAAGTGAGGTCTATCTTTGAAAAGTGGCAGAAAAAGAAATAAGCAGAGATGGTGCCAGTGC	1143
Db	61	GAAGTGAGGTCTATCTTTGAAAAGTGGCAGAAAAAGAAATAAGCAGAGATGGTGCCAGTGC	120
QY	1144	AGTGGCTTGCCACTCAAAAGAAAGGCAGCAGACAAAGTCGTCTTCTCTTTTCCAAATGACG	1203
Db	121	AGTGGCTTGCCACTCAAAAGAAAGGCAGCAGACAAAGTCGTCTTCTCTTTTCCAAATGACG	180
QY	1204	TCNACAGTGTGTGCATGGTACCTGTGTCAGAGCGAGGGCAGTCCCAAGTGAAGACTCTC	1263
Db	181	TCNACAGTGTGTGCATGGTACCTGTGTCAGAGCGAGGGCAGTCCCAAGTGAAGACTCTC	240
QY	1264	AGACCTCTTCCCTTCCCTTTAACTTTTCGACGTGATCTAAGAAGCCAGATTTCATC	1323
Db	241	AGACCTCTTCCCTTCCCTTTAACTTTTCGACGTGATCTAAGAAGCCAGATTTCATC	300
QY	1324	TGCACAAATACGTGGTGTGTACTTTTAGAGAGATTGATACAAAAGACGATTACAAATGCTC	1383
Db	301	TGCACAAATACGTGGTGTGTACTTTTAGAGAGATTGATACAAAAGACGATTACAAATGCTC	360
QY	1384	TCAGTGTCTGCCCCCAAGTACCACCTTCATGAAGAGTGCACCTGCTTTTCTGTGCAGAACTTC	1443
Db	361	TCAGTGTCTGCCCCCAAGTACCACCTTCATGAAGAGTGCACCTGCTTTTCTGTGCAGAACTTC	420
QY	1444	TCCATGTCAAGCAGCAGGTGTGCAGCAGGAAAAAGATCACAGGCTGCACGATGGCTGTCT	1503

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Db 421 TCATGTCAAGTAGCAGGTGTGTCAGCAGGAAAAGATCAACAAGCTGCCAGCATGGCTGT 480
Qy 1504 GCTCCTTTAGCCACCACCATGAGAACAGACAGACCTTAAGGCTTCTATCCACCAATT 1563
Db 481 GCTCCTTTAGCCACCACCATGAGAACAGACAGACCTTAAGGCTTCTATCCACCAATT 540
Qy 1564 ACAGGG-AAAAACGTTGATGAT-CCTGAAGCTTACTATGACGCTCAACAACAGCCTTA 1621
Db 541 ACAGGAAAAAAGCGTGTGATGATCCTGAAGCTTACTATGACGCTCAACAACAGCCTTA 600
Qy 1622 GTAATTAAACATTTTATACCAATAAAATTTTCAAAATATTACTAACTA 1669
Db 601 GTAATAAAA--CATTTTATCCAATAAAATTTCAAAATTTTGCTTAATA 646

RESULT 13
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LOCUS bb40e05.y1 NIH MGC 12 Homo sapiens cDNA clone IMAGE:2985728 5',
DEFINITION similar to TR.043844 O43844 IL-17 RECEPTOR. ;, mRNA sequence.
ACCESSION AW675096.1 GI:7540331
VERSION AW675096
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: bb40e05.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 441.
Location/Qualifiers
1..561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2985728"
/clone_lib="NIH MGC 12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/Note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."
BASE COUNT 146 a 143 c 141 g 130 t 1 others
ORIGIN
Query Match 30.3%; Score 554.2; DB 10; Length 561;
Best Local Similarity 99.3%; Pred. No. 7.4e-86;
Matches 556; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CGCGGATGCTGCTGCTGATAGAGCTGGCGCGCTGTGCAGGAGCGGCTACCCCGAG 60
Db 2 CGCGGATGCTGCTGCTGCTGATAGAGCTGGCGCGCTGTGCAGGAGCGGCTACCCCGAG 61
Qy 61 AGCCGACCGTTCATGCTGGCTCTGAACATGGGCGCATCTCCAGAGTGGATGCTACACATG 120
Db 62 AGCCGACCGTTCATGCTGGCTCTGAACATGGGCGCATCTCCAGAGTGGATGCTACACATG 121
Qy 121 ATCTAATCCCGAGACTTTGAGGAGCCTCCGAGTAGAACTGTTACAACTAGTTGCAAA 180
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Db 122 ATCTAATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTGTACAACTAGTTGCAAA 181
Qy 181 CAGGGGACTATTCAATTTTGTATGAATGAAGCTGGTACTCCGGCAGATGCCAGCATCC 240
Db 182 CAGGGGACTATTCAATTTTGTATGAATGAAGCTGGTACTCCGGCAGATGCCAGCATCC 241
Qy 241 GCTTGTGAAGGCCACCAAGATTTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGT 300
Db 242 GCTTGTGAAGGCCACCAAGATTTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGT 301
Qy 301 GTGTGAGTGCATATACACAGAGGCTTCCAGACTCAGACAGACCCCTCTGTGTGTAAT 360
Db 302 GTGTGAGTGCATATACACAGAGGCTTCCAGACTCAGACAGACCCCTCTGTGTGTAAT 361
Qy 361 GGACATTTTCCATATCGGCTTCCCTGTAGAGCTCAACACAGCTCTATTTCATTGGGGCCC 420
Db 362 GGACATTTTCCATATCGGCTTCCCTGTAGAGCTCAACACAGCTCTATTTCATTGGGGCCC 421
Qy 421 ATAATATTCTTAATCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 480
Db 422 ATAATATTCTTAATCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 481
Qy 481 CACAGGCTGCCTAGACACACATATGAATATAAAAAAGTGTGTCAAGGCCGGAGGCC 540
Db 482 CACAGGCTGCCTAGACACACATATGAATATAAAAAAGTGTGTCAAGGCCGGAGGCC 541
Qy 541 TGTGGGATCCGAACATCACT 560
Db 542 TGTGGGATCCGAACATCACT 561

RESULT 14
AW299271/c
LOCUS xs48h02.xl NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2772915 3',
DEFINITION mRNA sequence.
ACCESSION AW299271
VERSION AW299271.1 GI:6708948
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 510)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
Location/Qualifiers
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/lab_host="DH10B"
/Note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
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from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

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Best Local Similarity 99.0%; Pred. No. 5.3e-76;
Matches 500; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 30 GATAATGCAACATAAAGCATCTTC 6

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VERSION BF110326.1 GI:10940016
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

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found through the I.M.A.G.E.B. Consortium/LNL, send email to: info@image.lnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 470.

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FEATURES
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modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT      132 a      84 c      113 g      180 t
ORIGIN
Query Match      27.0%; Score 493; DB 12; Length 509;
Best Local Similarity 98.0%; Pred. No. 2.6e-75;
Matches 499; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:34:39 ; Search time 204.956 Seconds
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	1509.2	82.6	1515	9	US-10-174-590-399
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ALIGNMENTS

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; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; PRIORITY FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: prim transcript
; OTHER INFORMATION: cdna of human Evi27
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RESULT 2

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 ; Patent No. US20020037524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Medlock, Eugene
 ; APPLICANT: Yeh, Richard
 ; APPLICANT: Silbiger, Scott M.
 ; APPLICANT: Elliot, Gary S.
 ; APPLICANT: Nguyen, Hung Q.
 ; APPLICANT: Jing, Shuqian
 ; TITLE OF INVENTION: Lu-17 Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/37128B
 ; CURRENT APPLICATION NUMBER: US/09/886,404
 ; CURRENT FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: 09/810,384
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/266,159
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/213,125
 ; PRIOR FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 1841
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (50)..(1555)
 US-09-886-404-17

Query Match 97.8%; Score 1786; DB 10; Length 1841;
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Qy	1561	ATTACAG	GGAAAA	ACG	TGTGA	TGAT	CTCTG	AAGCTT	ACTATG	CAGCCT	CAAAA	CAGCCTT	1620
Db	1605	ATTACAG	GGAAAA	ACG	TGTGA	TGAT	CTCTG	AAGCTT	ACTATG	CAGCCT	CAAAA	CAGCCTT	1664
Qy	1621	AGTAAT	TAAAA	CA	TTTTAT	ACCA	TAAAA	TTTT	CAAA	TATTTA	CTAA	CTATG	1680
Db	1665	AGTAAT	TAAAA	CA	TTTTAT	ACCA	TAAAA	TTTT	CAAA	TATTTA	CTAA	CTATG	1724
Qy	1681	ACTAAC	CGATT	GGAA	ACTCAT	TTTAC	AACT	CTCA	AAAGCT	TGTTTTA	TACAT	AGAAAT	1740
Db	1725	ACTAAC	CGATT	GGAA	ACTCAT	TTTAC	AACT	CTCA	AAAGCT	TGTTTTA	TACAT	AGAAAT	1784
Qy	1741	CAGCTT	TAAAT	TGAAA	ACTGT	TAA	ACC	ATTTT	TGTA	TATG	CAACA	ATAA	1794
Db	1785	CAGCTT	TAAAT	TGAAA	ACTGT	TAA	ACC	ATTTT	TGTA	TATG	CAACA	ATAA	1838

RESULT 3
118-09-96

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RESULT 3
US-09-863-818A-1
; Sequence 1, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1509)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (46)..()
; OTHER INFORMATION:
; US-09-863-818A-1

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Query Match		97.7%	Score 1785.6	DB 9	Length 1796	
Best Local Similarity		99.8%	Pred. No. 0			
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Qy	3	GCGATGTCGCTCGCTGATAGGCTGGCGCGCTGTGCGAGGCGCGTACCCCGAGAG	62			
Db	1	GCGATGTCGCTCGCTGCTAAAGCTGGCGCGCTGTGCGAGGCGCGTACCCCGAGAG	60			
Qy	63	CCGACCGTTCAATGTGGCTCTGAACTGGGCACTCTCCAGATGGATGCTTACAACATGAT	122			
Db	61	CCGACCGTTCAATGTGGCTCTGAACTGGGCACTCTCCAGATGGATGCTTACAACATGAT	120			
Qy	123	CTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAACTGTTCACACTAGTGTGCAACA	182			
Db	121	CTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAACTGTTCACACTAGTGTGCAACA	180			
Qy	183	GGGACCTATTCAATTTTGTATGATGTAAGCTGGGTACTCCGGCGAGATGCCAGATCCGC	242			
Db	181	GGGACCTATTCAATTTTGTATGATGTAAGCTGGGTACTCCGGCGAGATGCCAGATCCGC	240			
Qy	243	TTGTTGAAGCCCAACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCTGT	302			
Db	241	TTGTTGAAGCCCAACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCTGT	300			
Qy	303	GTGAGTGCATTTACACAGAGGCTTCCAGACTCAGACAGAGCCCTCTGGTGGTAAATGG	362			
Db	301	GTGAGTGCATTTACACAGAGGCTTCCAGACTCAGACAGAGCCCTCTGGTGGTAAATGG	360			
Qy	363	ACATTTTCTTATATCGGCTTCCCTGTAGAGTGAACACAGCTCTATTTTCAATGGGGCCAT	422			
Db	361	ACATTTTCTTATATCGGCTTCCCTGTAGAGTGAACACAGCTCTATTTTCAATGGGGCCAT	420			
Qy	423	AATATTCTTAATCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACTCA	482			
Db	421	AATATTCTTAATCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACTCA	480			
Qy	483	CCAGGTGCTTAGACACACATAATGAATATAAAAAAAGTGTCTCAAGGCCGGAAGCCTG	542			
Db	481	CCAGGTGCTTAGACACACATAATGAATATAAAAAAAGTGTCTCAAGGCCGGAAGCCTG	540			
Qy	543	TGGGATCCGAACATCACTGCTGTAGAGATGAGGAGACAGTGAAGTGAATTTCA	602			
Db	541	TGGGATCCGAACATCACTGCTGTAGAGATGAGGAGACAGTGAAGTGAATTTCA	600			
Qy	603	ACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACACTATCATCGGGTT	662			
Db	601	ACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACACTATCATCGGGTT	660			
Qy	663	TCTCAGGTGTTGAGCCACACAGAGAGAAACAAACCGAGCTTCACTGTGATTCAGTG	722			
Db	661	TCTCAGGTGTTGAGCCACACAGAGAGAGAAACAAACCGAGCTTCACTGTGATTCAGTG	720			
Qy	723	ACTGGGATGATGAGGCTGCTAGGCTGCTGAGCTGCTTATTTCTTACTTGTGCGAGC	782			
Db	721	ACTGGGATGATGAGGCTGCTAGGCTGCTGAGCTGCTTATTTCTTACTTGTGCGAGC	780			
Qy	783	GACTGATCCGACATAAGAGAAAGTGTGCTCTGCCCAACAGAGCGCTCCCTTTCCCT	842			
Db	781	GACTGATCCGACATAAGAGAAAGTGTGCTCTGCCCAACAGAGCGCTCCCTTTCCCT	840			
Qy	843	CTGGATTAACAAACAAAGAGCGGAGGCTGGCTGCTCTCTCTCTGTCTCTGTCTG	902			
Db	841	CTGGATTAACAAACAAAGAGCGGAGGCTGGCTGCTCTCTCTCTGTCTCTGTCTG	900			
Qy	903	GTGGCCACATGGTGTGTGGAGGATCTATCTAATGTGGAGGCAACAAAGGATCAAG	962			
Db	901	GTGGCCACATGGTGTGTGGAGGATCTATCTAATGTGGAGGCAACAAAGGATCAAG	960			
Qy	963	AAGACTTCTCTTTTACACACACACTACTGCCCCCCTAATTAAGTCTTGTGGTTACCCA	1022			
Db	961	AAGACTTCTCTTTTACACACACACTACTGCCCCCCTAATTAAGTCTTGTGGTTACCCA	1020			

Qy	1023	TCTGAAATATGTTTCCATCACAAATTTGTTACTTCTCACTGAATTTCTTCAAAACCAATTGC	1082
Db	1021	TCTGAAATATGTTTCCATCACAAATTTGTTACTTCTCACTGAATTTCTTCAAAACCAATTGC	1080
Qy	1083	AGAAGTGAGGTGATCTCTGAAAGTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1142
Db	1081	AGAAGTGAGGTGATCTCTGAAAGTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1140
Qy	1143	CAGTGGCTTGGCCACTCAAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1202
Db	1141	CAGTGGCTTGGCCACTCAAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1200
Qy	1203	GTCAACAGTGTGTGCGATGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	1262
Db	1201	GTCAACAGTGTGTGCGATGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	1260
Qy	1263	CAAGACCTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT	1322
Db	1261	CAAGACCTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT	1320
Qy	1323	CTGCACAAATACGTGGTGTCTTCTTACGAGATTTGATACAAAGAGAGAGAGAGAGAGAG	1382
Db	1321	CTGCACAAATACGTGGTGTCTTCTTACGAGATTTGATACAAAGAGAGAGAGAGAGAG	1380
Qy	1383	CTCAGTGTCTGCCCCCAAGTACCACTTTCATGAAGGATGCGCACTGCTTCTGTGCGAGAACT	1442
Db	1381	CTCAGTGTCTGCCCCCAAGTACCACTTTCATGAAGGATGCGCACTGCTTCTGTGCGAGAACT	1440
Qy	1443	CTTCAATGTCAGCAGCAGGTGTGTCAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1502
Db	1441	CTTCAATGTCAGCAGCAGGTGTGTCAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1500
Qy	1503	TGCTCTCTGTCAGCCCAAGTACCACTTTCATGAAGGATGCGCACTGCTTCTGTGCGAGAACT	1562
Db	1501	TGCTCTCTGTCAGCCCAAGTACCACTTTCATGAAGGATGCGCACTGCTTCTGTGCGAGAACT	1560
Qy	1563	TACAGGAG	1622
Db	1561	TACAGGAG	1620
Qy	1623	TAAATTAACATTTTATACCAATTAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAA	1682
Db	1621	TAAATTAACATTTTATACCAATTAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAA	1680
Qy	1683	TAAACATTTGAAATACATTTTACAACTTCAAAAGCTGTTTATACATAGAAATCAATTTACA	1742
Db	1681	TAAACATTTGAAATACATTTTACAACTTCAAAAGCTGTTTATACATAGAAATCAATTTACA	1740
Qy	1743	GCTTTAATTTGAAATCACTTAAACATTTTGAATGATGCAACAAATTAAGCATCTTC	1794
Db	1741	GCTTTAATTTGAAATCACTTAAACATTTTGAATGATGCAACAAATTAAGCATCTTC	1792

RESULT 4
 US-09-886-404-19
 ; Sequence 19, Application US/09886404
 ; Patent No. US20020037524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Medlock, Eugene
 ; APPLICANT: Yeh, Richard
 ; APPLICANT: Silbiger, Scott M.
 ; APPLICANT: Elliot, Gary S.
 ; APPLICANT: Nguyen, Hung Q.
 ; APPLICANT: Jing, Shugian
 ; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/37128B
 ; CURRENT APPLICATION NUMBER: US/09/886.404
 ; CURRENT FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: 09/810,384
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/266,159
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/213,125

; PRIOR FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 19
 ; LENGTH: 2015
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (50)..(1729)
 US-09-886-404-19

Query Match 85.0%; Score 1552.4; DB 10; Length 2015;
 Best Local Similarity 89.3%; Pred. No. 0;
 Matches 1758; Conservative 0; Mismatches 36; Indels 174; Gaps 1;

Qy	1	CGGCGATGTCGCTCGCTGATTAAGCCTCGCGCGCTGTGCGAGGCGCGCTACCCCGAG	60
Db	45	CGGCGATGTCGCTCGCTGATTAAGCCTCGCGCGCTGTGCGAGGCGCGCTACCCCGAG	104
Qy	61	AGCCGACCGCTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACACATG	120
Db	105	AGCCGACCGCTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACACATG	164
Qy	121	ATCTAATCCCGAGACTTGGAGGAGCTCGAGTAGAACTCTGTTCAACTAGTGTGCAA	180
Db	165	ATCTAATCCCGAGACTTGGAGGAGCTCGAGTAGAACTCTGTTCAACTAGTGTGCAA	224
Qy	181	CAGGGAGCTATTCAATTTGATGAATGTAAGCTGGGTACTCCGGGCGAGATGCCAGCATC	240
Db	225	CAGGGAGCTATTCAATTTGATGAATGTAAGCTGGGTACTCCGGGCGAGATGCCAGCATC	284
Qy	241	GCTTGTGTAAGGCCACCAAGATTGTGTGACGGGCCAAAGCACTTCCAGTCTCTACAGCT	300
Db	285	GCTTGTGTAAGGCCACCAAGATTGTGTGACGGGCCAAAGCACTTCCAGTCTCTACAGCT	344
Qy	301	GTGTGAGTGTCAATATACACAGAGCCCTTCCAGACT	335
Db	345	GTGTGAGGCTGAGTGTGAGTGTGCGATCATGGCTCGCTCGGACCTCAATCTTCTGGGCT	404
Qy	336	-----	335
Db	405	CAAGCATCGTTCTGCTTCAAGCTCCCGAGCGCTGGGACTCGAGGCTGGGCGCACAGA	464
Qy	336	-----	335
Db	465	CTGGCTAATTTTGTAGTTTGTAGAGGGGGTTTCCACCGTGTGCTGGTCTTGAAT	524
Qy	336	-----CAGACCAAGCCCTCTGCTGTGTTGAATGACAT	366
Db	525	CCAGTGTCTCAGGCGATCTGCTCGCTCGGCTTCCCAAGTGTGCGATTACAGTGGACAT	584
Qy	367	TTTCTTATATCGGCTTCCCTGTAGAGCTGAACACAGCTCTATTTCATTTGGGGCCCAATA	426
Db	585	TTTCTTATATCGGCTTCCCTGTAGAGCTGAACACAGCTCTATTTCATTTGGGGCCCAATA	644
Qy	427	TTCTTAATGCAATATGAATGAAGTGGCCCTTCCATGTCTGTGAATTTTCACTCCACAG	486
Db	645	TTCTTAATGCAATATGAATGAAGTGGCCCTTCCATGTCTGTGAATTTTCACTCCACAG	704
Qy	487	GCTGCTAGACCAATAATGAATATAAAAAAAGTGTGTCAAGGCGGGAAGCTGTGGG	546
Db	705	GCTGCTAGACCAATAATGAATATAAAAAAAGTGTGTCAAGGCGGGAAGCTGTGGG	764
Qy	547	ATCCGAACTACTGTTGTAAGAATGAGGAGACAGTGTAGAGTGAAGTGAACCTTCAACCA	606
Db	765	ATCCGAACTACTGTTGTAAGAATGAGGAGACAGTGTAGAGTGAAGTGAACCTTCAACCA	824
Qy	607	CTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACAGCTATCATCGGGTTTCTC	666
Db	825	CTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACAGCTATCATCGGGTTTCTC	884
Qy	667	AGGTGTTTGAGCCACACAGAGAAACAAACCGGAGCTTTCAGTGTGATTCCAGTGACTG	726

Db	885	AGGTGTTTGAGCCACACAGAGAAACAAACGCGAGCTTCAGTGTGATTCCAGTGACTG	944
Qy	727	GGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTTACTTGTGTGCGAGCT	786
Db	945	GGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTTACTTGTGTGCGAGCT	1004
Qy	787	GCATCCGACATAAAGAACAGTGTGTCTGCGCCCAAAACAGGCGTCCCTTTCCCTCTGG	846
Db	1005	GCATCCGACATAAAGAACAGTGTGTCTGCGCCCAAAACAGGCGTCCCTTTCCCTCTGG	1064
Qy	847	ATAACAAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	906
Db	1065	ATAACAAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1124
Qy	907	CCACATGGGTGCTGTGGCGAGGATCTATCTAATGTGAGGCGACGAAAGGATCAAGAGAA	966
Db	1125	CCACATGGGTGCTGTGGCGAGGATCTATCTAATGTGAGGCGACGAAAGGATCAAGAGAA	1184
Qy	967	CTTCTTTTCTACCAACACACATCTGCGCCCGCCATTAAGTTCCTGTGTGTATACCATCTG	1026
Db	1185	CTTCTTTTCTACCAACACACATCTGCGCCCGCCATTAAGTTCCTGTGTGTATACCATCTG	1244
Qy	1027	AAATATGTTTCCATCACAAATTTGTTTACTTCACTGAAATTTCTTCAAAACCATTCAGAA	1086
Db	1245	AAATATGTTTCCATCACAAATTTGTTTACTTCACTGAAATTTCTTCAAAACCATTCAGAA	1304
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Db	1305	GTGAGTCTATCTTCAAAAGTGGCAGAAAGAAATAAGCAGAGATGGGTCCAGTGCAGT	1364
Qy	1147	GGCTTGGCACTCAAAAGAGGCGAGCAAAAGTCTTCTTCTTCAATAGCTCA	1206
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Db	1425	ACAGTGTGCGATGTTTCTGAGTGTGCGAGGCGAGGCGAGTCCAGTGAGAACTCTCAAG	1484
Qy	1267	ACCTCTTCCCTTCTGCTTAACTTCTGAGTGTGCGAGTGTGCGAGGCGAGTCCAGTGC	1326
Db	1485	ACCTCTTCCCTTCTGCTTAACTTCTGAGTGTGCGAGTGTGCGAGGCGAGTCCAGTGC	1544
Qy	1327	ACAAATAGCTGTGTGTCTACTTTAGAGAGATTGATACAAAGACGATTAACAATCTCA	1386
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Qy	1387	GTGTCTGCGCCCAAGTACCACTTTCATGAGGATGCGCACTGCTTCTGTGCGAGAACTCTCC	1446
Db	1605	GTGTCTGCGCCCAAGTACCACTTTCATGAGGATGCGCACTGCTTCTGTGCGAGAACTCTCC	1664
Qy	1447	ATGTCAAGCAGCAGGTGTCTCAGCAGGAAAGAAAGATCAAGCCTGCCACGATGGCTGTCT	1506
Db	1665	ATGTCAAGCAGCAGGTGTCTCAGCAGGAAAGAAAGATCAAGCCTGCCACGATGGCTGTCT	1724
Qy	1507	CCTTGTAGCCCACTTACAGAGAGAGACCTTAAAGGCTTCTTATCCCAATTA	1566
Db	1725	CCTTGTAGCCCACTTACAGAGAGAGACCTTAAAGGCTTCTTATCCCAATTA	1784
Qy	1567	GGGAAAAACAGTGTGATGATCTCTGAGCTTACTATGCGAGCTTACAAAGCCTTAGTAAT	1626
Db	1785	GGGAAAAACAGTGTGATGATCTCTGAGCTTACTATGCGAGCTTACAAAGCCTTAGTAAT	1844
Qy	1627	TAAACATTTTATCAATATAAATTTTCAATATTTTAACTTAATAGTACATTAACATAC	1686
Db	1845	TAAACATTTTATCAATATAAATTTTCAATATTTTAACTTAATAGTACATTAACATAC	1904
Qy	1687	GATTGGAACTACATTTTCAACTTCAAGCTTCTTTTATACATAGAAATCAATACAGCTT	1746
Db	1905	GATTGGAACTACATTTTCAACTTCAAGCTTCTTTTATACATAGAAATCAATACAGCTT	1964
Qy	1747	TAAATGAAACTGTAACTTTTGTATTAATGCAACAAATAAGCATCTTC	1794

Db 542 TGTGGATCCGACATCATCTGTTGTAAGAGATGAGAGACAGTAGAAGTAACTTCA 601
Qy 601 CAACCACTCCCTCGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGTT 660
Db 602 CAACCACTCCCTCGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGTT 661
Qy 661 TTTCTCAGGTGTTGAGCCACACACCAAGAAACAAACGCGCTTCAGTGGTGTCCAG 720
Db 662 TTTCTCAGGTGTTGAGCCACACACCAAGAAACAAACGCGCTTCAGTGGTGTCCAG 721
Qy 721 TGACTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCATATTTCTACTTTGGGCA 780
Db 722 TGACTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCATATTTCTACTTTGGGCA 781
Qy 781 GGAATGATCCGACATAAAGAAACAGTTGTGCTCTGCCCAACAAACAGCGCTCCCTTTCC 840
Db 782 GCGACTGCATCCGACATAAAGAAACAGTTGTGCTCTGCCCAACAAACAGCGCTCCCTTTCC 841
Qy 841 CTCTGATTAACAAACAAACGCGGAGGTGGCTGCTCTCTCTCTCTCTCTCTCTCTGC 900
Db 842 CTCTGATTAACAAACAAACGCGGAGGTGGCTGCTCTCTCTCTCTCTCTCTCTCTGC 901
Qy 901 TGGTGCCACATGGGTGCTGGGAGGATCTATCTAATGTGGAGGCACGAAAGGATCA 960
Db 902 TGGTGCCACATGGGTGCTGGGAGGATCTATCTAATGTGGAGGCACGAAAGGATCA 961
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Db 1022 CATCTGAATATGTTTCCATACACAAATTTGTTACTTCACTGAATTTCTTCAAAACATT 1081
Qy 1081 GCAGAGTCAGGTCTCTTTGAAAGTGCAGAAAGAAATAGCAGAGATGGGTCAG 1140
Db 1082 GCAGAGTCAGGTCTCTTTGAAAGTGCAGAAAGAAATAGCAGAGATGGGTCAG 1141
Qy 1141 TGCAGTGGCTTGCCTCAAAAGAGGAGCAGACAAAGTCGTCTTCTTTTCCAATG 1200
Db 1142 TGCAGTGGCTTGCCTCAAAAGAGGAGCAGACAAAGTCGTCTTCTTTTCCAATG 1201
Qy 1201 AGTCACAGTGTGCGATGTTACTGTCGCAAGAGGAGGAGTCAGTGGAGAACT 1260
Db 1202 AGTCACAGTGTGCGATGTTACTGTCGCAAGAGGAGGAGTCAGTGGAGAACT 1261
Qy 1261 CTCAGACCTCTTCCCTTGCCTTTAACTTTCTGCAAGTCTTAAGAGCCAGATTC 1320
Db 1262 CTCAGACCTCTTCCCTTGCCTTTAACTTTCTGCAAGTCTTAAGAGCCAGATTC 1321
Qy 1321 ATCTGCAAAATACGTGGTGGTCTACTTTAGAGAGATTGATCAAAAGACGATTACAATG 1380
Db 1322 ATCTGCAAAATACGTGGTGGTCTACTTTAGAGAGATTGATCAAAAGACGATTACAATG 1381
Qy 1381 CTCTCAGTGTGCCCCAAGTACCACTCATGAAGATGCCACTGTTCTTGTGCAAGAC 1440
Db 1382 CTCTCAGTGTGCCCCAAGTACCACTCATGAAGATGCCACTGTTCTTGTGCAAGAC 1441
Qy 1441 TTTCTCAGTGTGCCCCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
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Qy 1501 GCTGCTCTCTTTAG 1514
Db 1502 GCTGCTCTCTTTAG 1515

RESULT 6

US-10-000-157-11

; Sequence 11, Application US/10000157

; Publication No. US20020182673A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vanden, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P.Wickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1CIP4 (US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/253646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836


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; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-747-259-11

Query Match      82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGGCGATGTCGTGCTGCTGATAAGCCTGGCGCGCTGTGCGAGGAGCGCGGTACCCCGAG 60
Db 2 CGGCGATGTCGTGCTGCTGCTGATAAGCCTGGCGCGCTGTGCGAGGAGCGCGGTACCCCGAG 61
Qy 61 AGCCGACCGTTCATAGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTTACAACATG 120
Db 62 AGCCGACCGTTCATAGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTTACAACATG 121
Qy 121 ATCTAATCCCGGAGACTTTGAGGGACCTCCGAGTAGAACCTGTTACACTAGTGTGCAA 180
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Db 1202 ACCTCAACAGTGTGTCGGTGTACCTGTGGCAAGAGCGAGGCGAGTCCAGTGAGAACT 1261
Qy 1261 CTCAGAGACCTTTCCCTTGGCTTTTAACTTTTCTGCGAGTGATCTAAGAAGCCAGATTC 1320
Db 1262 CTCAGAGACCTTTCCCTTGGCTTTTAACTTTTCTGCGAGTGATCTAAGAAGCCAGATTC 1321
Qy 1321 ATCTGCAGAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGAGGATTACAATG 1380
Db 1322 ATCTGCAGAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGAGGATTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCCAAGTACCCTTCATGAAGATGCCACTGCTTTCTGTGCAGAAAC 1440
Db 1382 CTCTCAGTGTCTGCCCCAAGTACCCTTCATGAAGATGCCACTGCTTTCTGTGCAGAAAC 1441
Qy 1441 TTCTCCATGTCAGCAGCAGGTGTCTCAGCAGGAAAGATCACAAGCCTGCCAGATGGCT 1500
Db 1442 TTCTCCATGTCAGCAGCAGGTGTCTCAGCAGGAAAGATCACAAGCCTGCCAGATGGCT 1501
Qy 1501 GCTGCTCTCTGTAG 1514
Db 1502 GCTGCTCTCTGTAG 1515

RESULT 9
US-10-174-590-399
; Sequence 399, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RLC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PENDING FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCGCATGTCGTCTGTGTGATAAGCCTGGCGCGCTGTGCGAGGCGCGGTACCCCGAG 60
Db 2 CGCGCATGTCGTCTGTGTGATAAGCCTGGCGCGCTGTGCGAGGCGCGGTACCCCGAG 61
Qy 61 AGCCAGCGCTCAATGTGGCTCTGAACTGGGCGCATCTCCAGAGTGGATGCTACAAATG 120
Db 62 AGCCAGCGCTCAATGTGGCTCTGAACTGGGCGCATCTCCAGAGTGGATGCTACAAATG 121
Qy 121 ATCTAATCCCGGAGACTTGGGACCTCCGAGTAGAAGCTGTTCACTAGTGTGCAA 180
Db 122 ATCTAATCCCGGAGACTTGGGACCTCCGAGTAGAAGCTGTTCACTAGTGTGCAA 181
Qy 181 CAGGGGACTATTCAATTTTGTGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 240
Db 182 CAGGGGACTATTCAATTTTGTGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 241
Qy 241 GCTTGTGAAGCCCAACAGATTTGTGTGAACGGGCAAGCAACTTCCAGTCTCTACAGCT 300
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Db 242 GCTTGTGAAGCCCAACAGATTTGTGTGACGGGCAAGCAACTTCCAGTCTCTACAGCT 301
Qy 301 GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTCAGACAGAGCCCTCTGTGGTAAAT 360
Db 302 GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTCAGACAGAGCCCTCTGTGGTAAAT 361
Qy 361 GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAAACAAGTCTATTTTCAATTTGGGGCC 420
Db 362 GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAAACAAGTCTATTTTCAATTTGGGGCC 421
Qy 421 ATAAATTTCTTATATCGAATATGAATGAAGTGGCCCTTCCATGTCTGTGAATTTCACT 480
Db 422 ATAAATTTCTTATATCGAATATGAATGAAGTGGCCCTTCCATGTCTGTGAATTTCACT 481
Qy 481 CACAGGCTGCTTACACACATAATATAAATAAAGTGTGTCAAGGCGCGAAGCC 540
Db 482 CACAGGCTGCTTACACACATAATATAAATAAAGTGTGTCAAGGCGCGAAGCC 541
Qy 541 TGTGGATCCGAAACATCACTGCTTGTAAAGAAATGAGGAGACAGTAGAAGTGAATTTCA 600
Db 542 TGTGGATCCGAAACATCACTGCTTGTAAAGAAATGAGGAGACAGTAGAAGTGAATTTCA 601
Qy 601 CAACCACTCCCTGGGAAACAGATACATGGCTTTATCCAAACAGACACTATCATCGGGT 660
Db 602 CAACCACTCCCTGGGAAACAGATACATGGCTTTATCCAAACAGACACTATCATCGGGT 661
Qy 661 TTTCTCAGGTGTTGAGGCCACACAGAGAAACAAACGAGCTTTCAGTGGTGAATTTCCAG 720
Db 662 TTTCTCAGGTGTTGAGGCCACACAGAGAAACAAACGAGCTTTCAGTGGTGAATTTCCAG 721
Qy 721 TGACTGGGATAGTCAAGGTGCTACGGTGCAGCTCACTTCAATATTTTCTTCTGTGGCA 780
Db 722 TGACTGGGATAGTCAAGGTGCTACGGTGCAGCTCACTTCAATATTTTCTTCTGTGGCA 781
Qy 781 GCGACTGCATCCGACATATAAGGAACAGTGTGCTCTGCCACAAACAGGCGTCCCTTTCC 840
Db 782 GCGACTGCATCCGACATATAAGGAACAGTGTGCTCTGCCACAAACAGGCGTCCCTTTCC 841
Qy 841 CTCTGGATAACAAACAAAGAGCGGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 842 CTCTGGATAACAAACAAAGAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 901
Qy 901 TGGTGGCCACATGGGTGCTGGTGGCAGGAGTCTATCTAATGTGGAGGACGCAAGAGATCA 960
Db 902 TGGTGGCCACATGGGTGCTGGTGGCAGGAGTCTATCTAATGTGGAGGACGCAAGAGATCA 961
Qy 961 AGAAGACTTCTTTTCTACACACACTACTGCCCCCCTTAAGGTTCCTTGTGGTTTACC 1020
Db 962 AGAAGACTTCTTTTCTACACACACTACTGCCCCCCTTAAGGTTCCTTGTGGTTTACC 1021
Qy 1021 CATCTGAATATGTTTCCATCACACAAATTTGTTACTTCACTGAATTTCTTCAAAACCAT 1080
Db 1022 CATCTGAATATGTTTCCATCACACAAATTTGTTACTTCACTGAATTTCTTCAAAACCAT 1081
Qy 1081 GCAGAAGTGAGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAG 1140
Db 1082 GCAGAAGTGAGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAG 1141
Qy 1141 TGCAGTGGCTTGCCTCAAAAGAGGAGCAGACAAAGTGTCTTCTTCTTCTTCAATG 1200
Db 1142 TGCAGTGGCTTGCCTCAAAAGAGGAGCAGACAAAGTGTCTTCTTCTTCTTCAATG 1201
Qy 1201 AGCTCAACAGTGTGGCTGCTGCTGTCAGAGGAGGAGGAGTCCAGTAGAGAACT 1260
Db 1202 AGCTCAACAGTGTGGCTGCTGCTGTCAGAGGAGGAGGAGTCCAGTAGAGAACT 1261
Qy 1261 CTCAGAGACTTCTTCCCTTTCCTTTTAACTTTTCTGAGTGTATTAAGAGAGCCAGATTC 1320
Db 1262 CTCAGAGACTTCTTCCCTTTCCTTTTAACTTTTCTGAGTGTATTAAGAGAGCCAGATTC 1321
Qy 1321 ATCTGCAAAATAGTGTGGTGTCTTCTTGTAGAGATTTGATACAAAGACGATTTCAATG 1380
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Db 1322 ATCTGCACAAATACGTGGTGTCTACTTTAGAGAGATTGATCAAAAGACGATTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCCAAGTAGTACCACTTCATGAAGGATGCCACTGTTTCTGTGCAGAAC 1440
Db 1382 CTCTCAGTGTCTGCCCCAAGTAGTACCACTTCATGAAGATGCCACTGTTTCTGTGCAGAAC 1441
Qy 1441 TTCTCAGTGTCTGCCCCAAGTAGTACCACTTCATGAAGATGCCACTGTTTCTGTGCAGAAC 1500
Db 1442 TTCTCAGTGTCTGCCCCAAGTAGTACCACTTCATGAAGATGCCACTGTTTCTGTGCAGAAC 1501
Qy 1501 GCTGCTCTCTGTAG 1514
Db 1502 GCTGCTCTCTGTAG 1515

RESULT 10

US-10-176-758-399
; Sequence 399, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;
Matches 151; Conservative 0;

Qy 1 CGCGGATGTCGTCTGTGATAGCTGCGCGCGCTGTGCAGGAGCGCGTACCCCGAG 60
Db 2 CGCGGATGTCGTCTGTGATAGCTGCGCGCGCTGTGCAGGAGCGCGTACCCCGAG 61
Qy 61 AGCGGACGTTCAATGTGCTCTGAACCTGGGCGCATCTCCAGAGTGATGCTACAACTG 120
Db 62 AGCGGACGTTCAATGTGCTCTGAACCTGGGCGCATCTCCAGAGTGATGCTACAACTG 121
Qy 121 ATCTAATCCCGAGACTTGGAGGACCTCCGAGTAGAACCTGTACAACTAGTTTGCAA 180
Db 122 ATCTAATCCCGAGACTTGGAGGACCTCCGAGTAGAACCTGTACAACTAGTTTGCAA 181
Qy 181 CAGGGGACTATTCAATTTTGTAGTAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGTCC 240
Db 182 CAGGGGACTATTCAATTTTGTAGTAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGTCC 241
Qy 241 GCTTGTGAGGCGCCACAGATTGTGTGACCGGCAAGGAACTTCCAGTCTTACAGCT 300
Db 242 GCTTGTGAGGCGCCACAGATTGTGTGACCGGCAAGGAACTTCCAGTCTTACAGCT 301
Qy 301 GTGTGAGGTGCAATTACACAGAGGCGCTTCCAGACTCAGACACAGACCCCTCTGGTGGTAAAT 360
Db 302 GTGTGAGGTGCAATTACACAGAGGCGCTTCCAGACTCAGACACAGACCCCTCTGGTGGTAAAT 361
Qy 361 GGACATTTTCTATATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGGCC 420

Db 362 GGACATTTTCTATATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGGCC 421
Qy 421 ATAATATTCTTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 480
Db 422 ATAATATTCTTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 481
Qy 481 CACCAGGCTGCTAGACACACATAATGAAATATAAAAAAAGTGTCAAGCGCGGAAGCC 540
Db 482 CACCAGGCTGCTAGACACACATAATGAAATATAAAAAAAGTGTCAAGCGCGGAAGCC 541
Qy 541 TGTGGATCCGAAACATCTGCTTGTGAAGAAATGAGGAGACAGTAGAAGTGAACCTTCA 600
Db 542 TGTGGATCCGAAACATCTGCTTGTGAAGAAATGAGGAGACAGTAGAAGTGAACCTTCA 601
Qy 601 CAACCACTCCCTCGGAAACAGATACATGGCTCTTATCCAAACACAGCACTATCATCGGCT 660
Db 602 CAACCACTCCCTCGGAAACAGATACATGGCTCTTATCCAAACACAGCACTATCATCGGCT 661
Qy 661 TTTCTCAGGTGTTTGTAGCCACACAGAAAGAAACAAACCGAGCTTTCAGTGTGATTCAG 720
Db 662 TTTCTCAGGTGTTTGTAGCCACACAGAAAGAAACAAACCGAGCTTTCAGTGTGATTCAG 721
Qy 721 TGACTGGGATAGTGAAGTGTCTAGCGTGAGCTGACATTCATATTTTCTTACTTGTGGCA 780
Db 722 TGACTGGGATAGTGAAGTGTCTAGCGTGAGCTGACATTCATATTTTCTTACTTGTGGCA 781
Qy 781 CGCACTGCATCCGACATAAAGGAAACAGTGTCTGCTGCCCAACAAACAGGCGTCCCTTTCC 840
Db 782 CGCACTGCATCCGACATAAAGGAAACAGTGTCTGCTGCCCAACAAACAGGCGTCCCTTTCC 841
Qy 841 CTCTGGATAACAAACAAAGCCGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 842 CTCTGGATAACAAACAAAGCCGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 901
Qy 901 TGTGGCCACATGGGTGTGTGGCAGGATCTATCTAATGTGGAGGACCAAGAGGATCA 960
Db 902 TGTGGCCACATGGGTGTGTGGCAGGATCTATCTAATGTGGAGGACCAAGAGGATCA 961
Qy 961 AGAAGACTTCTCTTCTACCAACACACTACTGCCCCCATTAAGTTCTTGTGGTTTACC 1020
Db 962 AGAAGACTTCTCTTCTACCAACACACTACTGCCCCCATTAAGTTCTTGTGGTTTACC 1021
Qy 1021 CATCTGAAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAATT 1080
Db 1022 CATCTGAAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAATT 1081
Qy 1081 GCAGAGTGAGGTCAATCTTGAAGTGCGAGAAAGAAAGAAATAGCAGAGATGGGTCCAG 1140
Db 1082 GCAGAGTGAGGTCAATCTTGAAGTGCGAGAAAGAAAGAAATAGCAGAGATGGGTCCAG 1141
Qy 1141 TGCAGTGGCTTGGCACTCAAAAGAGGACGACAGCAAAAGTCTTCTCTTCTTCTTCTTCTTCT 1200
Db 1142 TGCAGTGGCTTGGCACTCAAAAGAGGACGACAGCAAAAGTCTTCTCTTCTTCTTCTTCTTCT 1201
Qy 1201 ACCTCAACAGTGTGTGCGATGTTACCTTGTGAGGAGGAGGAGGAGTCCAGTGAAGT 1260
Db 1202 ACCTCAACAGTGTGTGCGATGTTACCTTGTGAGGAGGAGGAGGAGTCCAGTGAAGT 1261
Qy 1261 CTCAAGACTCTTCTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
Db 1262 CTCAAGACTCTTCTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1321
Qy 1321 ATCTGCACAAATAGTGGTGTCTACTTTTAGAGATTTGATACAAAAGACGATTACAATG 1380
Db 1322 ATCTGCACAAATAGTGGTGTCTACTTTTAGAGATTTGATACAAAAGACGATTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCCAAGTACCACTTTCATGAAGGATGCCACTGCTTTCTGTGAGAAC 1440
Db 1382 CTCTCAGTGTCTGCCCCAAGTACCACTTTCATGAAGGATGCCACTGCTTTCTGTGAGAAC 1441
Qy 1441 TTCTCCATGTCAAGCAGAGTGTCAAGGAGGAAAGATCAAGCCCTGCCACGATGGCT 1500

Db 1442 TTCTCCATGTCAAGCAGCAGGTGTCTAGCAGGAAAGATCACAAGCCTGCCACGATGGCT 1501
Qy 1501 GCTGCTCCTTTGTAG 1514
Db 1502 GCTGCTCCTTTGTAG 1515

RESULT 11
US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred No. 0;
Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCGGATGCGTGTGCTGATGAAGCTGGCGCGGTGTGCGAGGCGCGCTACCCCGAG 60
Db 2 CGCGGATGCGTGTGCTGCTGAAGCTGGCGCGGTGTGCGAGGCGCGCTACCCCGAG 61
Qy 61 AGCGGACGCTTCAATGTGGCTCTGAAGCTGGCGCATCTCCAGAGTGGATGCTACAACTG 120
Db 62 AGCGGACGCTTCAATGTGGCTCTGAAGCTGGCGCATCTCCAGAGTGGATGCTACAACTG 121
Qy 121 ATCTAATCCCGAGACTTGAAGGACCTCCGAGTAGAAGCTGTACAACTAGTGTGCA 180
Db 122 ATCTAATCCCGAGACTTGAAGGACCTCCGAGTAGAAGCTGTACAACTAGTGTGCA 181
Qy 181 CAGGGGACTATTCAATTTTGTATGAATGTAAAGCTGGGTACTCCGGGAGATGCCAGCATCC 240
Db 182 CAGGGGACTATTCAATTTTGTATGAATGTAAAGCTGGGTACTCCGGGAGATGCCAGCATCC 241
Qy 241 GCTTGTGAAGGCCACCAAGATTGTGTGACGGGCAAGAACTTCCAGTCTTCAAGCT 300
Db 242 GCTTGTGAAGGCCACCAAGATTGTGTGACGGGCAAGAACTTCCAGTCTTCAAGCT 301
Qy 301 GTGTGAGTGGCAATTTACACAGAGGCTTCCAGACTCAGACAGACCTCTGGTGGTAAAT 360
Db 302 GTGTGAGTGGCAATTTACACAGAGGCTTCCAGACTCAGACAGACCTCTGGTGGTAAAT 361
Qy 361 GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCC 420
Db 362 GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCC 421
Qy 421 ATAATATTTCTTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTAATTTCACT 480
Db 422 ATAATATTTCTTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTAATTTCACT 481
Qy 481 CACCAAGGCTGTAGACCAATATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 540
Db 482 CACCAAGGCTGTAGACCAATATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 541

RESULT 12
US-10-175-737-399
; Sequence 399, Application US/10175737

Qy 541 TGTGGATCCGAACATCACTGCTTGTAAAGAAATGAGGAGACAGTAGAAGTGAACCTTCA 600
Db 542 TGTGGATCCGAACATCACTGCTTGTAAAGAAATGAGGAGACAGTAGAAGTGAACCTTCA 601
Qy 601 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCACACAGCACTATATCGGGT 660
Db 602 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCACACAGCACTATATCGGGT 661
Qy 661 TTTCTCAGGTGTTTGGAGCCACACAGAAAGAAACAAACGCGAGCTTTCAGTGGTGAATCCAG 720
Db 662 TTTCTCAGGTGTTTGGAGCCACACAGAAAGAAACAAACGCGAGCTTTCAGTGGTGAATCCAG 721
Qy 721 TGACTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTTACTTGTGGA 780
Db 722 TGACTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTTACTTGTGGA 781
Qy 781 GCGACTGCATCCGACATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 840
Db 782 GCGACTGCATCCGACATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 841
Qy 841 CTCTGGATAACAAACAAAGCAGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 842 CTCTGGATAACAAACAAAGCAGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 901
Qy 901 TGGTGGCCACATGGTGTGCTGGCAGGATCTATCTAATGTGGAGGACGAAAGATCA 960
Db 902 TGGTGGCCACATGGTGTGCTGGCAGGATCTATCTAATGTGGAGGACGAAAGATCA 961
Qy 961 AGAAGACTTCTTTTCTACCAACACACTACTGCCCCCCTTAAGGTTCTTGTGGTTTACC 1020
Db 962 AGAAGACTTCTTTTCTACCAACACACTACTGCCCCCCTTAAGGTTCTTGTGGTTTACC 1021
Qy 1021 CATCTGAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAT 1080
Db 1022 CATCTGAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAT 1081
Qy 1081 GCAGAAGTGAGTCACTCTTGAAGAGTGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGTCCAG 1140
Db 1082 GCAGAAGTGAGTCACTCTTGAAGAGTGGCAAGAAAGAAAGAAAGAAAGAAAGTCCAG 1141
Qy 1141 TGCAGTGGCTTGGCACTCAAGAGGAGCAGACAGAGTGGTCTTCTTCTTCTTCTTCTTCT 1200
Db 1142 TGCAGTGGCTTGGCACTCAAGAGGAGCAGACAGAGTGGTCTTCTTCTTCTTCTTCTTCT 1201
Qy 1201 AGCTCAACAGTGTGCGATGGTACTCTGTGCAAGAGCAGGAGGAGTCCAGTGAGAACT 1260
Db 1202 AGCTCAACAGTGTGCGATGGTACTCTGTGCAAGAGCAGGAGGAGTCCAGTGAGAACT 1261
Qy 1261 CTCAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
Db 1262 CTCAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1321
Qy 1321 ATCTGCAAAATACGTGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
Db 1322 ATCTGCAAAATACGTGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1381
Qy 1381 CTCTCAGTGTCTGCCCCCAAGTACCACTTCTGAGAGTGGCCTCTTCTTCTGTCAGAAC 1440
Db 1382 CTCTCAGTGTCTGCCCCCAAGTACCACTTCTGAGAGTGGCCTCTTCTTCTGTCAGAAC 1441
Qy 1441 TTCTCCATGTCAAGCAGCAGGTGTGTCAGGAGAAAGATCAAGCCTGCCACGATGGCT 1500
Db 1442 TTCTCCATGTCAAGCAGCAGGTGTGTCAGGAGAAAGATCAAGCCTGCCACGATGGCT 1501
Qy 1501 GCTGCTCCTTTGTAG 1514
Db 1502 GCTGCTCCTTTGTAG 1515

Db	782	GC GACTCGATCCGACATAAAGGAACAAGTTGTGCTCTGCCCAAAAACAGGCGTCCCTTTCCC	841
Qy	841	CTCTGGATAACAACAAAGCAAGCAGCGGAGGCTGGCTGCTCTCTCTCTGCTGTCTCTGTC	900
Db	842	CTCTGGATAACAACAAAGCAAGCAGCGGAGGCTGGCTGCTCTCTCTCTGCTGTCTCTGTC	901
Qy	901	TGTTGGCCACATGGTGCTGTGGTGGCAGGGATCTATCTAAATGTGGAGGCACGAAAGGATCA	960
Db	902	TGTTGGCCACATGGTGCTGTGGTGGCAGGGATCTATCTAAATGTGGAGGCACGAAAGGATCA	961
Qy	961	AGAAGACTTCCTTTTCTACACACACTACTGCCCCCCTTAAGGTTCTTTGTTGGTTTACC	1020
Db	962	AGAAGACTTCCTTTTCTACACACACTACTGCCCCCCTTAAGGTTCTTTGTTGGTTTACC	1021
Qy	1021	CATCTGAATATGTTTTCATCATCACAAATTGTTTACTTCTCAATCTGAA'TTCTTTCAAAACCA'CTT	1080
Db	1022	CATCTGAATATGTTTTCATCATCACAAATTGTTTACTTCTCAATCTGAA'TTCTTTCAAAACCA'CTT	1081
Qy	1081	GCAGAGTGAGGTCATCTTTGAAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAG	1140
Db	1082	GCAGAGTGAGGTCATCTTTGAAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAG	1141
Qy	1141	TGCAGTGGCTTGGCACTCAAAGAGAGGCAGCAGACAAAGTCGTCTTCTTTTCCAATG	1200
Db	1142	TGCAGTGGCTTGGCACTCAAAGAGAGGCAGCAGACAAAGTCGTCTTCTTTTCCAATG	1201
Qy	1201	ACGTCAACAGTGTGCGATGGTAGCTGTGGCAAGCGAGGGCAGTCCCAGTGAGAACT	1260
Db	1202	ACGTCAACAGTGTGCGATGGTAGCTGTGGCAAGCGAGGGCAGTCCCAGTGAGAACT	1261
Qy	1261	CTCAAGACCTCTTTCCCCCTTGGCCTTTAACTTTCTGCACTGATCTAAGAACCCAGATTC	1320
Db	1262	CTCAAGACCTCTTTCCCCCTTGGCCTTTAACTTTCTGCACTGATCTAAGAACCCAGATTC	1321
Qy	1321	ATTGCAACAAATACGTGGTGGTCTACTTTTAGAGAGATTGATACAAAGACGATTACAATG	1380
Db	1322	ATTGCAACAAATACGTGGTGGTCTACTTTTAGAGAGATTGATACAAAGACGATTACAATG	1381
Qy	1381	CTCTCAGTGTCTGCCCCAAGTACCCTTCATCAAGATGCCACTGCTTTCTGTGCAGAAC	1440
Db	1382	CTCTCAGTGTCTGCCCCAAGTACCCTTCATCAAGATGCCACTGCTTTCTGTGCAGAAC	1441
Qy	1441	TTCTCCATGTCAAGCAGCAGGTGTCTAGCAGGAAAAAGATCAAGCTGCCACGATGGCT	1500
Db	1442	TTCTCCATGTCAAGCAGCAGGTGTCTAGCAGGAAAAAGATCAAGCTGCCACGATGGCT	1501
Qy	1501	GCTGCTCCTTGTAG 1514	
Db	1502	GCTGCTCCTTGTAG 1515	
RESULT 14			
US-10-173-706-399			
; Sequence 399, Application US/10173706			
; Publication No. US2003002293A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3430R1C7			
; CURRENT APPLICATION NUMBER: US/10/173,706			
; CURRENT FILING DATE: 2002-06-17			

; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-706-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCGCATGCGTGTGCTGATGAAGCTGGCGCGCTGTGCGAGGAGCGCGCTACCCCGAG 60
DB 2 CGCGCATGCGTGTGCTGATGAAGCTGGCGCGCTGTGCGAGGAGCGCGCTACCCCGAG 61
QY 61 AGCGGACGCTTCAATGTGCTCTGAAGCTGGGCGCATCTCCAGAGTGGATGCTACACATG 120
DB 62 AGCGGACGCTTCAATGTGCTCTGAAGCTGGGCGCATCTCCAGAGTGGATGCTACACATG 121
QY 121 ATCTAATCCCGGAGACTTTGAGGAGCTCCGAGTAGAAGCTGTTCACAACTAGTGTGCA 180
DB 122 ATCTAATCCCGGAGACTTTGAGGAGCTCCGAGTAGAAGCTGTTCACAACTAGTGTGCA 181
QY 181 CAGGGGACTATTCAATTTTGTGATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGCATCC 240
DB 182 CAGGGGACTATTCAATTTTGTGATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGCATCC 241
QY 241 GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCACTTCCAGTCTTACAGCT 300
DB 242 GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCACTTCCAGTCTTACAGCT 301
QY 301 GTGTGAGTGTCAATTAACAGAGGCTTCCAGACTCAGACAGACCTCTGTGTGTAAT 360
DB 302 GTGTGAGTGTCAATTAACAGAGGCTTCCAGACTCAGACAGACCTCTGTGTGTAAT 361
QY 361 GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAACAGCTATTTTCATTTGGGGGCC 420
DB 362 GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAACAGCTATTTTCATTTGGGGGCC 421
QY 421 ATAAATTTCTTAATGAATATGAATGAATGAGAGTGGCCCTTCCATGCTGTGAATTTCACT 480
DB 422 ATAAATTTCTTAATGAATATGAATGAATGAGAGTGGCCCTTCCATGCTGTGAATTTCACT 481
QY 481 CACCGGCTGCTTAGACCAATTAACAGAGGCTTCCAGACTCAGACAGGCTGTCAAGGCGGAGCC 540
DB 482 CACCGGCTGCTTAGACCAATTAACAGAGGCTTCCAGACTCAGACAGGCTGTCAAGGCGGAGCC 541
QY 541 TGTGGATCCGAACATCACTGCTTGTGAAGAATGAGAGAGAGTGAAGTGAAGTGAAGTGA 600
DB 542 TGTGGATCCGAACATCACTGCTTGTGAAGAATGAGAGAGAGTGAAGTGAAGTGAAGTGA 601
QY 601 CAACCACTCCCTGGGAAACAGATATGCTTCTTATCAACACAGCACTATCATCGGCT 660
DB 602 CAACCACTCCCTGGGAAACAGATATGCTTCTTATCAACACAGCACTATCATCGGCT 661
QY 661 TTTCTCAGGTGTTTGAAGCCACACAGAGGCTTCCAGGCTTCAAGTGTGATTTCCAG 720
DB 662 TTTCTCAGGTGTTTGAAGCCACACAGAGGCTTCCAGGCTTCAAGTGTGATTTCCAG 721
QY 721 TGACTGGGATAGTGAAGTGTGCTAGCGTCACTGCTTCAATTTTCTTACTTTGGCA 780
DB 722 TGACTGGGATAGTGAAGTGTGCTAGCGTCACTGCTTCAATTTTCTTACTTTGGCA 781
QY 781 GCGACTGCATCCGACATAAGGAACAGTGTGCTGTGCGCCACAAACAGCGCTCCCTTCC 840
DB 782 GCGACTGCATCCGACATAAGGAACAGTGTGCTGTGCGCCACAAACAGCGCTCCCTTCC 841
QY 841 CTCTGGATAACAAACAAAGCAAGCGGAGGTGGTGTCTCTCTCTGTGTCTCTGCG 900
DB 842 CTCTGGATAACAAACAAAGCAAGCGGAGGTGGTGTCTCTCTCTGTGTCTCTGCG 901
QY 901 TGGTGGCCACATGGGTGTGCTGGCAGGGATCTATCTAATGTGGAGGCAAGAGGATCA 960

DB 902 TGGTGGCCACATGGGTGTGCTGGCAGGATCTATCTAATGTGGAGGCAAGAGGATCA 961
QY 961 AGAAGACTTCTTTTCTTACCACCACTACTGCCCCCATTAAGGTCTTGTGGTTTACC 1020
DB 962 AGAAGACTTCTTTTCTTACCACCACTACTGCCCCCATTAAGGTCTTGTGGTTTACC 1021
QY 1021 CATCTGAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTCAAAACCAATT 1080
DB 1022 CATCTGAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTCAAAACCAATT 1081
QY 1081 GCAGAAGTGAAGTCTATCTTGAAGAGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAG 1140
DB 1082 GCAGAAGTGAAGTCTATCTTGAAGAGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAG 1141
QY 1141 TGCAGTGGCTTGCCTCACTCAAAAGAGGAGCAGAGCAAAAGTGTCTTCTTCTTCCAATG 1200
DB 1142 TGCAGTGGCTTGCCTCACTCAAAAGAGGAGCAGAGCAAAAGTGTCTTCTTCTTCCAATG 1201
QY 1201 AGCTCAACAGTGTGTGCGATGTGTACTTGTGCAAGAGGAGGCGAGTCCCACTGAGAACT 1260
DB 1202 AGCTCAACAGTGTGTGCGATGTGTACTTGTGCAAGAGGAGGCGAGTCCCACTGAGAACT 1261
QY 1261 CTCAAGACTTCTTCCCTTGCCTTTAACTTTCTGAGTGTATCTAAGAGCCAGATTC 1320
DB 1262 CTCAAGACTTCTTCCCTTGCCTTTAACTTTCTGAGTGTATCTAAGAGCCAGATTC 1321
QY 1321 ATCTGCACAAATACGTGTGTGTACTTTAGAGAGATGTACAAAAGACGATTACAATG 1380
DB 1322 ATCTGCACAAATACGTGTGTGTGTACTTTAGAGAGATGTACAAAAGACGATTACAATG 1381
QY 1381 CTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGATGCCACTGCTTTCTGTGCGAAGC 1440
DB 1382 CTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGATGCCACTGCTTTCTGTGCGAAGC 1441
QY 1441 TTCTCCATGTCAAGCAGCAGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
DB 1442 TTCTCCATGTCAAGCAGCAGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1501
QY 1501 GCTGCTCTCTGTAG 1514
DB 1502 GCTGCTCTCTGTAG 1515

RESULT 15
US-10-175-738-399
; Sequence 399, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10175,738
; PRIORITY FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-738-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCGCATGTCGCTCGTCTGCTGATAAGCCTGGCGCGCTGTGCGAGGCGCGGTACCCCGAG 60
Db CGCGCATGTCGCTCGTCTGCTGCTGATAAGCCTGGCGCGCTGTGCGAGGCGCGGTACCCCGAG 61

Qy 61 AGCGACCGTTCAATGTGGCTCTGAACTGGGCGCATCTCCAGAGTGGATGCTACAAATG 120
Db AGCGACCGTTCAATGTGGCTCTGAACTGGGCGCATCTCCAGAGTGGATGCTACAAATG 121

Qy 121 ATCTAATCCCGAGACTTTGAGGACCTCCGAGTAGAACTGTACAACTAGTGTGCAA 180
Db ATCTAATCCCGAGACTTTGAGGACCTCCGAGTAGAACTGTACAACTAGTGTGCAA 181

Qy 181 CAGGGGACTATTCAATTTTGATGAATGTAACTGGGTACTCCGGGCGAGATGCCAGATCC 240
Db CAGGGGACTATTCAATTTTGATGAATGTAACTGGGTACTCCGGGCGAGATGCCAGATCC 241

Qy 241 GCTTGTGAAGGCCACCAAGATTGTGTGAACGGGCAAAAGCAACTTCCAGTCTTACAGCT 300
Db GCTTGTGAAGGCCACCAAGATTGTGTGAACGGGCAAAAGCAACTTCCAGTCTTACAGCT 301

Qy 301 GTGTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACGACCCCTCTGGTGGTAAAT 360
Db GTGTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACGACCCCTCTGGTGGTAAAT 361

Qy 361 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAGCTATTTTCAATTTGGGGCCC 420
Db GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAGCTATTTTCAATTTGGGGCCC 421

Qy 421 ATAAATTTCTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 480
Db ATAAATTTCTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 481

Qy 481 CACCGGCTGCTAGACACATATGAATATATAAATAAGTGTGCAAGGCGGAGGCC 540
Db CACCGGCTGCTAGACACATATGAATATATAAATAAGTGTGCAAGGCGGAGGCC 541

Qy 541 TGTGGATCCGAACATCACTGTGTGAAGAAGATGAGGAGACAGTAGAAGTGAATCCA 600
Db TGTGGATCCGAACATCACTGTGTGAAGAAGATGAGGAGACAGTAGAAGTGAATCCA 601

Qy 601 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACACTATCATCGGT 660
Db CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACACTATCATCGGT 661

Qy 661 TTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGGGAGCTTCAGTGGTGAATCCAG 720
Db TTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGGGAGCTTCAGTGGTGAATCCAG 721

Qy 721 TGACTGGGATAGTGAAGTGTGCTGCTGAGTCACTCCATATTTTCTACTTGTGGCA 780
Db TGACTGGGATAGTGAAGTGTGCTGCTGAGTCACTCCATATTTTCTACTTGTGGCA 781

Qy 781 GCGACTGCATCCGACATAAGGAACAGTTGTCTGTGCCCAACAAACAGGCGTCCCTTTCC 840
Db GCGACTGCATCCGACATAAGGAACAGTTGTCTGTGCCCAACAAACAGGCGTCCCTTTCC 841

Qy 841 CTCTGGATTAACAAACAAACGCGGAGGCTGGTGGCTCTCTCTCTGTCTCTGTC 900
Db CTCTGGATTAACAAACAAACGCGGAGGCTGGTGGCTCTCTCTCTGTCTCTGTC 901

Qy 901 TGGTGGCCACATGGGTGCTGGTGGAGGATCTATCTAATGTGGAGGACGAAAGATCA 960
Db TGGTGGCCACATGGGTGCTGGTGGAGGATCTATCTAATGTGGAGGACGAAAGATCA 961

Qy 961 AGAAGACTTCTTTTCTACCAACACACTACTGCCCGCCCAATTAAGGTTCTTGTGGTTTACC 1020
Db AGAAGACTTCTTTTCTACCAACACACTACTGCCCGCCCAATTAAGGTTCTTGTGGTTTACC 1021

Qy 1021 CATCTGAAATATGTTTCCATCATCAAAATTTGTGTTACTTCACTGAAATTTCTTCAAAACCAATT 1080

Db 1022 CATCTGAAATATGTTTCCATCATCAAAATTTGTACTTCACTGAAATTTCTTCAAAACCAATT 1081
Qy 1081 GCAGAAAGTGAGGTCACTCTTGAAGAGTGCAGAAAAGAAAATAGCAGAGATGGGTCCAG 1140
Db 1082 GCAGAAAGTGAGGTCACTCTTGAAGAGTGCAGAAAAGAAAATAGCAGAGATGGGTCCAG 1141
Qy 1141 TGCAGTGGCTTGCCTCTCAAAAGAGGAGCAGACAAAGTCGTCTTCTTCTTCAATG 1200
Db 1142 TGCAGTGGCTTGCCTCTCAAAAGAGGAGCAGACAAAGTCGTCTTCTTCTTCAATG 1201
Qy 1201 AGCTCAACAGTGTGCGATGTGCTGTGGCAAGAGCGAGGCGAGTCCAGTGAGAACT 1260
Db 1202 AGCTCAACAGTGTGCGATGTGCTGTGGCAAGAGCGAGGCGAGTCCAGTGAGAACT 1261
Qy 1261 CTCAGAGCTTCTTCCCTTTCCTTTTAACTTTTCTGCAAGTCTTAAGAGCCAGATTC 1320
Db 1262 CTCAGAGCTTCTTCCCTTTCCTTTTAACTTTTCTGCAAGTCTTAAGAGCCAGATTC 1321
Qy 1321 ATCTGCAAAATACGTGGTGTCTACTTTTAGAGATTTGATACAAAAGACGATTTACAATG 1380
Db 1322 ATCTGCAAAATACGTGGTGTCTACTTTTAGAGATTTGATACAAAAGACGATTTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGATGCCACTGCTTTCTGTGCAGAAC 1440
Db 1382 CTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGATGCCACTGCTTTCTGTGCAGAAC 1441
Qy 1441 TTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAGATCAAGCCTGCCACGATGGCT 1500
Db 1442 TTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAGATCAAGCCTGCCACGATGGCT 1501
Qy 1501 GCTGCTCTTGTAG 1514
Db 1502 GCTGCTCTTGTAG 1515

Search completed: May 28, 2003, 10:35:25
Job time : 219.956 secs

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Matches 137; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 1551 TATCCACCAATTACAGGAAAAACGTGTGATGATCTCGAAGCTTACTATGACAGCCTTAC 1610
 1118 TATCTTACAACTCCCAAAAAAAGAACAGTACAAAGTACCTTAATATACAGGCTA 1177
 QY 1611 AAACAGCTTAGTATTAACATTTTATACCAATATAATTTTCAATATTTACTACTAA 1670
 1178 AAAAATGAGGTAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAAT 1237
 QY 1671 TGTAGCATTAACAGATTGGAAGTACATTTTACAACCTTCAAGCTGTTTATACATAG 1730
 1238 AAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAAT 1297
 Db 1731 AAATCAATTACAGCTTAAATGAAACTGTAAACCACTTTGATATAGCAACATTAACCAT 1790
 1298 AAATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1357
 QY 1791 CTTCACAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAAT 1827
 Db 1358 AAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAAT 1394

RESULT 2

US-08-487-826B-13
 ; Sequence 13, Application US/08487826B
 ; Patent No. 5993827
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Kim L.
 ; APPLICANT: Chitnis, Chetan
 ; APPLICANT: Miller, Louis H.
 ; APPLICANT: Peterson, David S.
 ; APPLICANT: Su, Xin-zhaun
 ; APPLICANT: Wellens, Thomas E.
 ; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 ; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe Martens Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,826B
 ; FILING DATE: 10-SEP-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israelsen, Ned
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: NIH121.001CPI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 235-8550
 ; TELEFAX: (619) 235-0176
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19124 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-487-826B-13

Query Match 2.7%; Score 50; DB 2; Length 19124;
 Best Local Similarity 51.8%; Pired. No. 0.0052;

Matches 113; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1609 ACAACAGCCTTAGTATTAAACATTTTATACCAATAAATTTTCAAAATATTACTACT 1668
 Db 15455 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15514
 QY 1669 AATGTAGCATTAACAGATTGGAACATCTTACCACTTCAAGCTGTTTATACAT 1728
 Db 15515 GGAGAAAAATTTTATAAAAAATATAAAAAATATAAAAAATATAAAAAATTTTATGATGATA 15574
 QY 1729 AGAATCAATTACAGCTTAAATGAAACTGTAAACCACTTTGATATAGCAACATTAAC 1788
 Db 15575 AAAAAAGAAAAAGATTAATCAAAAAATTTAAAAAATTTTATATATAAAAAATATA 15634
 QY 1789 ATCTCCAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATA 1826
 Db 15635 TTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15672

RESULT 3

US-08-655-352-10
 ; Sequence 10, Application US/08655352
 ; Patent No. 6077991
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachettira W. Poovaiah, Zhinua Liu,
 ; APPLICANT: Shameekumar Patil, Daisuke Takezawa
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ; ADDRESSEE: Whinston, LLP
 ; STREET: One World Trade Center
 ; STREET: 121 S.W. Salmon Street
 ; STREET: Suite 1600
 ; CITY: Portland
 ; STATE: Oregon
 ; COUNTRY: United States of America
 ; ZIP: 97204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3-1/2 inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/655,352
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/323,449
 ; FILING DATE: October 14, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dow, Alan E.
 ; REGISTRATION NUMBER: 35,123
 ; REFERENCE/DOCKET NUMBER: 4630-45000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1776 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double stranded
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; DESCRIPTION: Tobacco CcAMK cDNA and deduced amino-acid
 ; FEATURE:
 ; NAME/KEY: protein-coding sequence (not including
 ; NAME/KEY: stop codon)
 ; LOCATION: nucleotides 20-1570
 ; US-08-655-352-10

D0 1728 AA 1776

RESULT 5
US-09-257-825B-10
Sequence 10 Application US/09257825B
Patent No. 640352
GENERAL INFORMATION:
APPLICANT: Pooviah, Bachettira W.
APPLICANT: Patil, Shameekumar
APPLICANT: Takezawa, Daishuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
FILE REFERENCE: 4630-51993
CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 08/655,352
PRIOR FILING DATE: 1996-05-23
PRIOR APPLICATION NUMBER: US 60/014,743
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 1776
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-257-825B-10

Query Match 2.7% Score 49.8; DB 4; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.0021;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

D0 1719 TTTTATCATGAAATCAATTACAGCTTTAATTGAAAACGTGAACATTTGATTAATGCA 1778
D0 1668 TTTTATCAGTCAGTGTAAGATAAGATCCTTTAATTAATTGGAGACCTTTATGTA AAAA 1727

D0 1779 ACAATTAAGCATCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
D0 1728 AA 1776

RESULT 6
US-08-628-417-6
Sequence 6 Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158

Db 2748 ATTGTTATATATAATCTGAAATGTAAGTCTTTAAGTAATAAAAAAAAAAAAAAAAAAAAA 2807
Oy 1803 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827
Db 2808 AAAAAAAAAAAAAAAAAAAAAAAAAA 2832

RESULT 9

US-08-747-221B-26/c

; Sequence 26, Application US/08747221B

; Patent No. 6063610

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/747,221B

; FILING DATE: No. 6063610e1ember 12, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2836 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; US-08-747-221B-26

Query Match 2.7%; Score 49; DB 3; Length 2836;

Best Local Similarity 58.6%; Pred. No. 0.0042; Mismatches 60; Indels 0; Gaps 0;

Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 1683 TAACGATTGGAAGTCACTTTCACAACTGCTTTTATACATAGCAATCAATTACA 1742

Db 149 TATGATTATATGTCACATGTAATAATACAAATGCGGTGTTAAAAATATCTGTATTAA 90

Oy 1743 GCTTAAATGAAAGTGTACCATTTTGATTAATGCACATATAAGCATCTTCCAAAAA 1802

Db 89 ATTGTTATATATAATCTGAAATGTAAGTCTTTAAGTAATAAAAAAAAAAAAAAAAAAAAA 30

Oy 1803 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

US-09-005-051-24

; Sequence 24, Application US/09005051

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 629122e1 Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2836 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 99..1889

; US-09-005-051-24

Query Match 2.7%; Score 49; DB 4; Length 2836;

Best Local Similarity 58.6%; Pred. No. 0.0042; Mismatches 60; Indels 0; Gaps 0;

Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 1683 TAACGATTGGAAGTCACTTTCACAACTGCTTTTATACATAGCAATCAATTACA 1742

Db 2688 TATGATTATATGTCACATGTAATAATACAAATGCGGTGTTAAAAATATCTGTATTAA 2747

Oy 1743 GCTTAAATGAAAGTGTACCATTTTGATTAATGCACATATAAGCATCTTCCAAAAA 1802

Db 2748 ATTGTTATATATAATCTGAAATGTAAGTCTTTAAGTAATAAAAAAAAAAAAAAAAAAAAA 2807

Oy 1803 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827

Db 2808 AAAAAAAAAAAAAAAAAAAAAAAAAA 2832

US-09-005-051-26/c

; Sequence 26, Application US/09005051

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 629122e1 Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2836 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 99..1889

; US-09-005-051-24

Query Match 2.7%; Score 49; DB 4; Length 2836;

Best Local Similarity 58.6%; Pred. No. 0.0042; Mismatches 60; Indels 0; Gaps 0;

Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 1683 TAACGATTGGAAGTCACTTTCACAACTGCTTTTATACATAGCAATCAATTACA 1742

Db 2688 TATGATTATATGTCACATGTAATAATACAAATGCGGTGTTAAAAATATCTGTATTAA 2747

Oy 1743 GCTTAAATGAAAGTGTACCATTTTGATTAATGCACATATAAGCATCTTCCAAAAA 1802

Db 2748 ATTGTTATATATAATCTGAAATGTAAGTCTTTAAGTAATAAAAAAAAAAAAAAAAAAAAA 2807

Oy 1803 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827

Db 2808 AAAAAAAAAAAAAAAAAAAAAAAAAA 2832

US-09-005-051-26/c

; Sequence 26, Application US/09005051

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 629122e1 Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2836 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 99..1889

; US-09-005-051-24

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/494-9505
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-051-26

Query Match 2.7%; Score 49; DB 4; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0042;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1683 TAACGATTGAACTACATTACAACTCTGTTTATACATAGAAATCAATTACA 1742
DB 149 TATGATTAATGTCACATGTAATAATGCAATGCGGTTTAAATAATCTGATTTAA 90
QY 1743 GCTTAAATGAAACTGTAAACCTTTGATTAATGCAACATTAAGCATCTTCCAAAA 1802
DB 89 ATGTGATTAATTAATCTGATAATGACTTTTAAGTAAAAA 30
QY 1803 AAAAAAAAAAAAAAAAAAAAAA 1827
DB 29 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 12
US-08-242-677-1
Sequence 1, Application US/08242677
Patent No. 5677143
GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: and uses thereof in regulating Gene Expression and in the
NUMBER OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4863
US-08-242-677-1

Query Match 2.7%; Score 49; DB 1; Length 5173;
Best Local Similarity 69.1%; Pred. No. 0.0054;
Matches 67; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1731 AATCAATTACAGACTTTAATGAAACCTGATTTGATTAATGCAACATTAAGCAT 1790
DB 5059 AATTGATTTCTTCCTTAATAAATTTTAAGCATTTCCATTAATAAAAAAAAAAAAA 5118
QY 1791 CTTCAAAAAAAAAAAAAAAAAAAAA 1827
DB 5119 AAAAAAAAAAAAAAAAAAAAAA 5155

RESULT 13
US-09-014-969-14
Sequence 14, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Springer, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2447 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-014-969-14

Query Match
 Best Local Similarity 50.4%; Score 48.4; DB 2; Length 2447;
 Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1594 CTTACTATGACGCTTAAACAGCCTTAGTAATTAACATTTTATACCAATTAATTTT 1653
 DB 2214 CTTTAATGTGCAATTAACCTTTGGGAGAAAAAATTTTAAAAAATTTTAAAAA 2273
 QY 1654 CAATATTTCTAATGATGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1713
 DB 2274 AA 2333
 QY 1714 AGCTGTTTATCATGAAATCAATTAACGCTTAAATGAAACCTGTAACATTTGATA 1773
 DB 2334 AA 2393
 QY 1774 ATGCAACAATTAAGCATCTTCCAAAAAATTTTAAAAAATTTTAAAAA 1827
 DB 2394 AA 2447

RESULT 14

US-08-924-747-25
 Sequence 25, Application US/08924747
 Patent No. 6063570

GENERAL INFORMATION:
 APPLICANT: MCGONIGLE, BRIAN
 APPLICANT: O'KEEFE, DANIEL
 TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
 TITLE OF INVENTION: ENZYMES
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
 STREET: 1007 MARKET STREET
 CITY: WILMINGTON
 STATE: DELAWARE
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.50 INCH
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
 SOFTWARE: MICROSOFT WORD VERSION 7.0A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/924,747
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: FLOYD, LINDA AXAMETHY
 REGISTRATION NUMBER: 33,692
 REFERENCE/DOCKET NUMBER: CL-1108
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-773-0164
 TELEFAX: 302-773-0164
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 991 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 TISSUE TYPE: SOYBEAN
 IMMEDIATE SOURCE:
 CLONE: SSM.PK0067.G5
 US-08-924-747-25

Query Match
 Best Local Similarity 69.9%; Score 48.2; DB 3; Length 991;
 Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1735 CAATTACAGCTTTAATGAAAGTGAACCATTTTGATATGCAACAATTAAGCATCTTC 1794
 DB 891 CTAATTTTAATTTTAATGAAAGTGAACCATTTTGATATGCAACAATTAAGCATCTTC 1794
 QY 1795 CAAATTAATTTTAATGAAAGTGAACCATTTTGATATGCAACAATTAAGCATCTTC 1827
 DB 951 AA 983

RESULT 15

US-09-247-373B-25
 Sequence 25, Application US/09247373B
 Patent No. 6168954

GENERAL INFORMATION:
 APPLICANT: MCGONIGLE, BRIAN
 APPLICANT: O'KEEFE, DANIEL
 TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
 FILE REFERENCE: CL-1108-B
 CURRENT APPLICATION NUMBER: US/09/247,373B
 PRIOR FILING DATE: 1999-02-10
 PRIOR APPLICATION NUMBER: 08/924,747
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 25
 LENGTH: 991
 TYPE: DNA
 ORGANISM: SOYBEAN
 US-09-247-373B-25

Query Match
 Best Local Similarity 69.9%; Score 48.2; DB 4; Length 991;
 Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1735 CAATTACAGCTTTAATGAAAGTGAACCATTTTGATATGCAACAATTAAGCATCTTC 1794
 DB 891 CTAATTTTAATTTTAATGAAAGTGAACCATTTTGATATGCAACAATTAAGCATCTTC 1794
 QY 1795 CAAATTAATTTTAATGAAAGTGAACCATTTTGATATGCAACAATTAAGCATCTTC 1827
 DB 951 AA 983

Search completed: May 28, 2003, 10:19:18
 Job time: 165.735 secs

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Db 1621 ACTAATTAACCTTTTATACCATTAATAATTTTCAAAATTTACTACTATGATGACATTA 1680
Qy 1681 ACTAAGATTGGAACTACATTTTACCACTTCAAGCTGTTTATACATGAAATCATTA 1740
Db 1681 ACTAAGATTGGAACTACATTTTACCACTTCAAGCTGTTTATACATGAAATCATTA 1740
Qy 1741 CAGCTTAATTTGAAACTGTACATTTTGTATGATGCAACATTAAGCATTTTCCAAAA 1800
Db 1741 CAGCTTAATTTGAAACTGTACATTTTGTATGATGCAACATTAAGCATTTTCCAAAA 1800
Qy 1801 AAAAAAAAAAAAAAAAAAAAAA 1827
Db 1801 AAAAAAAAAAAAAAAAAAAAAA 1827

RESULT 2
AAD28776
ID AAD28776 standard; DNA; 1841 BP.
AC AAD28776;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.
XX
KW Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;
KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;
KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
KW eczema; psoriasis; wound healing; osteoporosis; Paget's disease;
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
KW cancer; diabetes; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..1558
FT /tag= a
FT /product= "Human IL-17RB-2 protein"
FT sig_peptide 50..92
FT /tag= b
FT mat_peptide 93..1555
FT /tag= c
FT /product= "Mature IL-17RB-2 protein"
XX
PN WO200208285-A2.
XX
PD 31-JAN-2002.
XX
PF 21-JUN-2001; 2001WO-US19861.
XX
PR 22-JUN-2000; 2000US-213125P.
PR 02-FEB-2001; 2001US-266159P.
PR 16-MAR-2001; 2001US-0810384.
XX
PA (AMGE-) AMGEN INC.
XX
PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;
XX
DR P-Psdb; AAE18127.
XX
DR WPI; 2002-155217/20.
XX
FT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
FT polypeptides useful in the treatment, prevention and diagnosis of
FT diseases e.g. cancer -
XX
PS Disclosure; Page 230-232; 242pp; English.
XX
CC The invention relates to nucleic acid molecules encoding Interleukin 17
CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels

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CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,
CC preventing or ameliorating a disease, such as immune system dysfunction
CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);
CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
CC disease, transplant rejection, graft vs. host disease); infections (HIV,
CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma
CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye
CC (blindness, retinal neuropathy) and treatment of diseases involving
CC inflammation. The present sequence is human Interleukin-17 receptor B-2
CC (IL-17RB-2) DNA.
XX
SQ Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;
XX
Query Match 97.8%; Score 1786; DB 24; Length 1841;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CGGCGATGTCGTCGCTGATTAACCTTGGCCGCTGTGACGAGCCGCCAATCCCGG 60
Db 45 CGGCGATGTCGTCGCTGCTAAACCTTGGCCGCTGTGACGAGCCGCCAATCCCGG 104
Qy 61 AGCCGACCGTCAATGATGAGCTCTGAACCTGGGCACTCTCCAGTGAATGATCAACATG 120
Db 105 AGCCGACCGTCAATGATGAGCTCTGAACCTGGGCACTCTCCAGTGAATGATCAACATG 164
Qy 121 ATCTAATCCCGGAGACTTGAAGGACCTCCGAGTAAACCTGTTCAACTAGTGTGCAA 180
Db 165 ATCTAATCCCGGAGACTTGAAGGACCTCCGAGTAAACCTGTTCAACTAGTGTGCAA 224
Qy 181 CAGGGGACTATTCATTTTGTATGAAATGTAAGTGGGTCTCGGGCAATGACACATCC 240
Db 225 CAGGGGACTATTCATTTTGTATGAAATGTAAGTGGGTCTCGGGCAATGACACATCC 284
Qy 241 GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCACTCCAGTCCCTACAGT 300
Db 285 GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCACTCCAGTCCCTACAGT 344
Qy 301 GTGTAGGATGCAATTACACAGAGGCTTCCAGACTCAGACCGCTCTGGTGGTAAT 360
Db 345 GTGTAGGATGCAATTACACAGAGGCTTCCAGACTCAGACCGCTCTGGTGGTAAT 404
Qy 361 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAACAGTCAATTTTCATGGGGCC 420
Db 405 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAACAGTCAATTTTCATGGGGCC 464
Qy 421 ATTAATATTCCTAATGCAATATGAAATGAGATGGCCCTTCCATGCTGTGAATTCACCT 480
Db 465 ATTAATATTCCTAATGCAATATGAAATGAGATGGCCCTTCCATGCTGTGAATTCACCT 524
Qy 481 CACCAGGCTGCTTGAAGCACAATATGAAATATTAATAAAGTGTCAAGGCCGGAAGCC 540
Db 525 CACCAGGCTGCTTGAAGCACAATATGAAATATTAATAAAGTGTCAAGGCCGGAAGCC 584
Qy 541 TGTGGATCCGAACATCACTGCTGTGAAGAGATGAGAGACAGTAGAAGTAACTTCA 600
Db 585 TGTGGATCCGAACATCACTGCTGTGAAGAGATGAGAGACAGTAGAAGTAACTTCA 644
Qy 601 CAACCACTCCCTGGGAAACAGATACATGAGCTTATCAACACAGCACTATCATCGGGT 660
Db 645 CAACCACTCCCTGGGAAACAGATACATGAGCTTATCAACACAGCACTATCATCGGGT 704
Qy 661 TTTCTCAGAGTGTGAGCACAACAGAAACAAACCGAGCTTCAAGTGTGATTTCCAG 720
Db 705 TTTCTCAGAGTGTGAGCACAACAGAAACAAACCGAGCTTCAAGTGTGATTTCCAG 764
Qy 721 TGACTGGGATAGTGAAGGTGCTACGCTGACGCTGATCTCATATTTTCTACTGTGGCA 780
Db 765 TGACTGGGATAGTGAAGGTGCTACGCTGACGCTGATCTCATATTTTCTACTGTGGCA 824

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QY 781 GCGACTGATCCGACATTAAGAAAGAGTTGCTCTGCCCCAAGAGGGGCTCCCTTTCC 840
DB 825 GCGACTGATCCGACATTAAGAAAGAGTTGCTCTGCCCCAAGAGGGGCTCCCTTTCC 884
QY 841 CTCTGGATTAACAACAAAGAGAGCGGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTC 900
DB 885 CTCTGGATTAACAACAAAGAGAGCGGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTC 944
QY 901 TGGTGGCCATGAGGCTGCTGCTGAGGAGATCTATCTATGAGGAGCAGAAAGATCA 960
DB 945 TGGTGGCCATGAGGCTGCTGCTGAGGAGATCTATCTATGAGGAGCAGAAAGATCA 1004
QY 961 AGAAGATTCCTCTTTCTACCAACAACACTACTGCCCCCATTAAGGTTCTGTGGTTACC 1020
DB 1005 AGAAGATTCCTCTTTCTACCAACAACACTACTGCCCCCATTAAGGTTCTGTGGTTACC 1064
QY 1021 CATCTGAATATGTTTCTTCAATCAACAATTTGTTACTTCACTGAATTTCTTCAAAACATT 1080
DB 1065 CATCTGAATATGTTTCTTCAATCAACAATTTGTTACTTCACTGAATTTCTTCAAAACATT 1124
QY 1081 GCAAGATGAGTGCATCTTGAAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1125 GCAAGATGAGTGCATCTTGAAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1184
QY 1141 TGCAGTGGCTTGGCCTCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1185 TGCAGTGGCTTGGCCTCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1244
QY 1201 ACCTCAACATGTTGTTGAGAGTGTACTGTGGCAAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1245 ACCTCAACATGTTGTTGAGAGTGTACTGTGGCAAGAGAGAGAGAGAGAGAGAGAGAG 1304
QY 1261 CTCGAAGACTCTTCTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
DB 1305 CTCGAAGACTCTTCTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1364
QY 1321 ATCTGCAACAATAGTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
DB 1365 ATCTGCAACAATAGTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1424
QY 1381 CTCTCAAGTCTGCTCCCAAGTATCACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1425 CTCTCAAGTCTGCTCCCAAGTATCACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1484
QY 1441 TTCTCCATGTCAGAGCAGAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1485 TTCTCCATGTCAGAGCAGAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1544
QY 1501 GCTGCTCTTGTAGCCCAAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1545 GCTGCTCTTGTAGCCCAAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1604
QY 1561 ATTACAGAGAGAGAGAGAGTGTGTGTCTTCAAGAGTGTCTTCAAGAGAGAGAG 1620
DB 1605 ATTACAGAGAGAGAGAGAGTGTGTGTCTTCAAGAGTGTCTTCAAGAGAGAGAG 1664
QY 1621 AGTAATTTAAACATTTTATCAATTAATTTTCAATTAATTTTCAATTAATTTTCA 1680
DB 1665 AGTAATTTAAACATTTTATCAATTAATTTTCAATTAATTTTCAATTAATTTTCA 1724
QY 1681 ACTAAGATTTGAAGATCAATTTCAACTTCAAGAGTGTGTGTCTTCAAGAGAGAG 1740
DB 1725 ACTAAGATTTGAAGATCAATTTCAACTTCAAGAGTGTGTGTCTTCAAGAGAGAG 1784
QY 1741 CAGCTTTAATTTGAAGATCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCA 1794
DB 1785 CAGCTTTAATTTGAAGATCAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCA 1838

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RESULT 3
ABR03200
ID ABR03200 standard; cDNA; 1841 BP.

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XX AC ABA03200;
XX 11-FEB-2002 (first entry)
DT 11-FEB-2002 (first entry)
XX 11-FEB-2002 (first entry)
DE Human IL-17 receptor like protein #1 coding sequence.
XX Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
XX antipsoriatic; antimicrobial; anorectic; neuroprotective;
XX antiaesthetic; antiallergic; dermatological; cytostatic; gene therapy;
XX interleukin 17; immune system disorder; infection; weight; reproductive;
XX neuronal dysfunction; lung; ascema; skin; eczema; kidney; inflammation;
XX glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
XX tumour; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 50..1558
FT /*tag= a
FT /product= "Human IL-17 receptor-like protein #1"
XX
XX WO200168705-A2.
XX
XX 20-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US08688.
XX
XX 16-MAR-2000; 2000US-189923P.
XX 12-MAY-2000; 2000US-204208P.
XX 27-NOV-2000; 2000US-072323P.
XX 02-FEB-2001; 2001US-266159P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;
XX P-PSDB; AM47456.
XX
XX WPI; 2002-055100/07.
XX
XX Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
XX polypeptides, useful for treating, diagnosing, ameliorating or
XX preventing immune system disorders (e.g. psoriatic arthritis) and
XX infections (e.g. viral infections) -
XX
XX Claim 1; Fig 1; 239pp; English.
XX
XX The present invention relates to novel human nucleic acids encoding
XX interleukin 17 (IL-17) receptor like proteins. The present sequence is
XX one such coding sequence. The IL-17 receptor-like proteins and coding
XX sequences are useful for treating a pathological condition related to
XX immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
XX viral infections), weight disorders (e.g. obesity), neuronal dysfunction
XX disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
XX disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
XX bone disease (e.g. osteoporosis), vascular system disorders (e.g.
XX ischaemia), eye disorders, reproductive disorders, tumours and
XX inflammation.
XX
XX Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;
SQ

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Query Match 97.8%; Score 1786; DB 24; Length 1841;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 CCGCGATGTCGCTGCTGCTGATTAAGCTTGGCCGCTGTGCAAGAGCCCGTACCCCGAG 60
DB 45 CCGCGATGTCGCTGCTGCTGATTAAGCTTGGCCGCTGTGCAAGAGCCCGTACCCCGAG 104
QY 61 AGCCGACGGTCAATGTTGGCTCTGAACCTGGGCGCATCTCCAGAGTGAAGTCAACATG 120
DB 105 AGCCGACGGTCAATGTTGGCTCTGAACCTGGGCGCATCTCCAGAGTGAAGTCAACATG 164

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Qy	121	ATCTAAATCCCGAGACTTGAAGGACCTCCGAGTAACACTGTTCCTCACTAATGTTGCA	180
Db	165	ATCTAAATCCCGAGACTTGAAGGACCTCCGAGTAACACTGTTCCTCACTAATGTTGCA	224
Qy	181	CAGGGGACTATTCAAATTTTGATGATAGTAAGCTGGGTACTCCGGGAGATGCGACATCC	240
Db	225	CAGGGGACTATTCAAATTTTGATGATAGTAAGCTGGGTACTCCGGGAGATGCGACATCC	284
Qy	241	GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCCAGTCTCAAGCT	300
Db	285	GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCCAGTCTCAAGCT	344
Qy	301	GTGTGAGTGCAAATTAACAAGAGCCCTCCAGACTGACACGACCCCTGTGGTGGTAAT	360
Db	345	GTGTGAGTGCAAATTAACAAGAGCCCTCCAGACTGACACGACCCCTGTGGTGGTAAT	404
Qy	361	GGAATATTTTCCCTATATCGGCTCCCTGTGAGCTGAACAAGTCTATTTCAATGGGGGCC	420
Db	405	GGAATATTTTCCCTATATCGGCTCCCTGTGAGCTGAACAAGTCTATTTCAATGGGGGCC	464
Qy	481	CACCAAGCTCCCTAGACCACTATATGAAATATTAATAAAAAAGTGTGCACAGGCCGGAAGCC	540
Db	525	CACCAAGCTCCCTAGACCACTATATGAAATATTAATAAAAAAGTGTGCACAGGCCGGAAGCC	584
Qy	541	TGTGGATTCGGAACATCATCTGCTTGTATGAGAATATAGGAGACAGTAAAGGAATCTTCA	600
Db	585	TGTGGATTCGGAACATCATCTGCTTGTATGAGAATATAGGAGACAGTAAAGGAATCTTCA	644
Qy	601	CAACCACTCCCTCGGAGAAACAGATACAGTGGCTTTATCCAAACAAGCACTATCATCGGGT	660
Db	645	CAACCACTCCCTCGGAGAAACAGATACAGTGGCTTTATCCAAACAAGCACTATCATCGGGT	704
Qy	661	TTTTCTCAGGTGTTTGAGCCACACCAAGAAACAAACCGGAGCTTCAGTGTGATTCAG	720
Db	705	TTTTCTCAGGTGTTTGAGCCACACCAAGAAACAAACCGGAGCTTCAGTGTGATTCAG	764
Qy	721	TGACTGGAGATAGTGAAGGAGTACAGGTGAGCTGACTCATATTTTCTCTATTTGAGCA	780
Db	765	TGACTGGAGATAGTGAAGGAGTACAGGTGAGCTGACTCATATTTTCTCTATTTGAGCA	824
Qy	781	GCGACTGCATCCGACATATTAAGGAAGCAAGTGTGCTCTGCCCAAAAACAGGCGTCCCTTCC	840
Db	825	GCGACTGCATCCGACATATTAAGGAAGCAAGTGTGCTCTGCCCAAAAACAGGCGTCCCTTCC	884
Qy	841	CTCTGTGAATTAACAACAAAAGCAGCCGGAGAGCTGCGTCTCTCTCTGCTGTCTTGC	900
Db	885	CTCTGTGAATTAACAACAAAAGCAGCCGGAGAGCTGCGTCTCTCTCTGCTGTCTTGC	944
Qy	901	TGTGTGGCAATGGGTGTGTGTGTGGGAGGATCTATCTAATGTGGAGGCAAGAAAGATCA	960
Db	945	TGTGTGGCAATGGGTGTGTGTGTGGGAGGATCTATCTAATGTGGAGGCAAGAAAGATCA	1004
Qy	961	AGAAAGCTTCCTTTCTTACACACACACTACTGCCCCCATTAAGGTTCTTGTGTTTACC	1020
Db	1005	AGAAAGCTTCCTTTCTTACACACACACTACTGCCCCCATTAAGGTTCTTGTGTTTACC	1064
Qy	1021	CATCTGAATATATGTTTTCATACACAATTTGTATCTTCACTGAATTTCTTCAAAACAT	1080
Db	1065	CATCTGAATATATGTTTTCATACACAATTTGTATCTTCACTGAATTTCTTCAAAACAT	1124
Qy	1081	GCACAAATGAGGTTCATCTCTTGAAATGTGCGAGAAAAGAAAATAGACAGATGGGTCCAG	1140
Db	1125	GCACAAATGAGGTTCATCTCTTGAAATGTGCGAGAAAAGAAAATAGACAGATGGGTCCAG	1184
Qy	1141	TGCAGTGGCTTGCACTCAAAAGAGGACAGACAACAATGCTCTTCTCTTCTTCAATG	1200
Db	1185	TGCAGTGGCTTGCACTCAAAAGAGGACAGACAACAATGCTCTTCTCTTCTTCAATG	1244
Qy	1201	ACGTCAACAGTGTGTGCGATGTATCCTTGGCAAGACGAGGGCACTCCAGTGAACCT	1260

Db	1245	ACGTCAACAGTGTGTGGCATGTACCTGTGGCAAGACGAGGGACATGCCAGTGAAGACT	1304
Qy	1261	CTCAAGACCTTCTCCCTTGGCTTAACTTTCTGACGTATCTAAGAAGCCAGATTC	1320
Db	1305	CTCAAGACCTTCTCCCTTGGCTTAACTTTCTGACGTATCTAAGAAGCCAGATTC	1364
Qy	1321	ATCTGCACAATTAAGTGTGTGTCTACTTTAGAGAGATTGATCAAAAAGAGATTACATG	1380
Db	1365	ATCTGCACAATTAAGTGTGTGTCTACTTTAGAGAGATTGATCAAAAAGAGATTACATG	1424
Qy	1381	CTCTCAGTGTGTGCCCAAGTACACTTCATGAAAGATGTGCACCTCTTCTGTGCAGAAC	1440
Db	1425	CTCTCAGTGTGTGCCCAAGTACACTTCATGAAAGATGTGCACCTCTTCTGTGCAGAAC	1484
Qy	1441	TTCTCCATGTTCAGACAGAGGTGTCAACAGAAAAAAGATCAACAAGCTGCACAGTGGCT	1500
Db	1485	TTCTCCATGTTCAGACAGAGGTGTCAACAGAAAAAAGATCAACAAGCTGCACAGTGGCT	1544
Qy	1501	GCTGCTCTCTGTAGCCCAACCCATGAGAAGACAGACCTTAAGGCTTCTATCCACCA	1560
Db	1545	GCTGCTCTCTGTAGCCCAACCCATGAGAAGACAGACCTTAAGGCTTCTATCCACCA	1604
Qy	1561	ATTACAGGAAAAAAGCGTGATGATCTCTAAGCTTACTATGACAGCTTCAACACGCTT	1620
Db	1605	ATTACAGGAAAAAAGCGTGATGATCTCTAAGCTTACTATGACAGCTTCAACACGCTT	1664
Qy	1621	AGTATATTAACATTTTATACCAATAAAATTTCAATATTTACTATCAATATGTAGCATTA	1680
Db	1665	AGTATATTAACATTTTATACCAATAAAATTTCAATATTTACTATCAATATGTAGCATTA	1724
Qy	1681	ACTACAGATTGGAAACTACATTTCACCTTCAAGGCTGTTTATATACATGAAATCAATTA	1740
Db	1725	ACTACAGATTGGAAACTACATTTCACCTTCAAGGCTGTTTATATACATGAAATCAATTA	1784
Qy	1741	CAGCTTATATGAAACCTGTAAACATTTTGATATGCAAGATTAACATCTTC	1794
Db	1785	CAGCTTATATGAAACCTGTAAACATTTTGATATGCAAGATTAACATCTTC	1838

RESULT 4

AA518126

ID AA518126 standard; cDNA; 1796 BP.

XX AA518126;

XX DT 26-MAR-2002 (first entry)

XX DE Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA.

XX KW Human; DNAX cytokine receptor subunit 6; DCRS6; phosphate labelling; ss;

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 4..1512

XX FT /*tag= a

XX FT /product= "Human DCRS6"

XX WO200190358-A2.

XX PN 29-NOV-2001.

XX PD 23-MAY-2001; 2001MO-US16767.

XX PR 24-MAY-2000; 2000US-206862P.

XX PA (SCHE) SCHERING CORP.

XX EI Gorman DM;

XX WP1; 2002-106198/14.

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1784

DR P-PSDB; AAU11351.
 XX Isolated antigenic human or mouse DNA receptor subunit-like
 PT polypeptide useful for detecting antibodies generated in response to
 PT presence of increased protein levels or immunological disorders -
 XX
 XX Disclosure; Page 7-10; 148bp; English.
 XX
 CC The invention relates to primate and rodent DNA cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies.
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents cDNA encoding the human
 CC DCRS6 polypeptide.
 XX
 SQ Sequence 1796 BP; 514 A; 439 C; 399 G; 444 T; 0 other;
 Query Match 97.7%; Score 1785.6; DB 24; Length 1796;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1788; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGATGTCGCTCGTGTGATTAAGCTGGCCGCTGTGCAAGAGCCGTAACCCGAGAG 62
 DB 1 GCGATGTCGCTCGTGTGATTAAGCTGGCCGCTGTGCAAGAGCCGTAACCCGAGAG 60
 QY 63 CCGACGCTTCAATGTGCTGTAAGCTGGCCATCTCCAGAGTGGATGTACAAACATGAT 122
 DB 61 CCGACGCTTCAATGTGCTGTAAGCTGGCCATCTCCAGAGTGGATGTACAAACATGAT 120
 QY 123 CTATATCCCGGAGACTTGAAGGACCTCCAGATAGAACCTGTACATAGTGTGCAACA 182
 DB 121 CTATATCCCGGAGACTTGAAGGACCTCCAGATAGAACCTGTGTACATAGTGTGCAACA 180
 QY 183 GGGGACATTCATTTTGAATGAATGTAAGTGGTACTCCGGGAGATGCGAGATCCGC 242
 DB 181 GGGGACATTCATTTTGAATGAATGTAAGTGGTACTCCGGGAGATGCGAGATCCGC 240
 QY 243 TTGTGGAAGCCACCAAGATTGTGTGACGGGCAAAAGCACTTCCAGTCTCAAGCTGT 302
 DB 241 TTGTGGAAGCCACCAAGATTGTGTGACGGGCAAAAGCACTTCCAGTCTCAAGCTGT 300
 QY 303 GTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACCCCTGTGTGTAATGG 362
 DB 301 GTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACCCCTGTGTGTAATGG 360
 QY 363 ACATTTTCCATATTCGGCTCCCTGTAGACTGAACCACTTATTTCAATTTGGGCCAT 422
 DB 361 ACATTTTCCATATTCGGCTCCCTGTAGACTGAACCACTTATTTCAATTTGGGCCAT 420
 QY 423 AATATTCCTATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACTCA 482
 DB 421 AATATTCCTATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACTCA 480
 QY 483 CCAAGCTGCTTGAACCAATATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 542
 DB 481 CCAAGCTGCTTGAACCAATATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
 QY 543 TGGGATCCGAAACATCACTGCTTGTGAAGAATGAAGAGACAGTAAGAGGAATTTTACA 602
 DB 541 TGGGATCCGAAACATCACTGCTTGTGAAGAATGAAGAGACAGTAAGAGGAATTTTACA 600
 QY 603 ACCACTCCCTGGGAAACAGATACATGGCTTTATCCACACAGCACTATCATCGGGTTT 662
 DB 601 ACCACTCCCTGGGAAACAGATACATGGCTTTATCCACACAGCACTATCATCGGGTTT 660
 QY 663 TCTCAGGTGTTTGAAGCCACACAGAAAGAAACAAACGCGAGCTTCAGTGTGATTCAGTG 722

DB 661 TCTCAGGTGTTTGAAGCCACACAGAAAGAAACAAACCGAGCTTCAGTGTGATTCAGTG 720
 QY 723 ACTGGGATATGTAAAGTGTCTAGGTGCACTGACTATTTTCTACTTGTGCAAG 782
 DB 721 ACTGGGATATGTAAAGTGTCTAGGTGCACTGACTATTTTCTACTTGTGCAAG 780
 QY 783 GACTGATCCGACATTAAGGAACAGTTGTGCTGTGCCCAAAACAGAGCCCTTCCCT 842
 DB 781 GACTGATCCGACATTAAGGAACAGTTGTGCTGTGCCCAAAACAGAGCCCTTCCCT 840
 QY 843 CTGGAATACAAACAAAGCAAGCCGGAGGCTGTGCTCTCTCTGTCTGTCTG 902
 DB 841 CTGGAATACAAACAAAGCAAGCCGGAGGCTGTGCTCTCTCTGTCTGTCTG 900
 QY 903 GTGGCCACATGGGTGTGTGTGGAGGATCTATATGTGAGAGACAAAGATCAAG 962
 DB 901 GTGGCCACATGGGTGTGTGTGGAGGATCTATATGTGAGAGACAAAGATCAAG 960
 QY 963 AAGACTTCTTTCTACACACACACTGACCCCATTAAGGATCTTGTGTTTACCA 1022
 DB 961 AAGACTTCTTTCTACACACACACTGACCCCATTAAGGATCTTGTGTTTACCA 1020
 QY 1023 TCTGAATATGTTTTCATACACAAATTTGTACTGATTAATTTCTTCAAAACATTC 1082
 DB 1021 TCTGAATATGTTTTCATACACAAATTTGTACTGATTAATTTCTTCAAAACATTC 1080
 QY 1083 AGAAGTAGGTATCTCTTGAAGAGTGGCAAGAAATAGCAGAGTGGTCCAGTG 1142
 DB 1081 AGAAGTAGGTATCTCTTGAAGAGTGGCAAGAAATAGCAGAGTGGTCCAGTG 1140
 QY 1143 CAGTGTCTGACCACTCAAAAGAGGACAGACAAAGTGTCTCTTCTTCAATGAC 1202
 DB 1141 CAGTGTCTGACCACTCAAAAGAGGACAGACAAAGTGTCTCTTCTTCAATGAC 1200
 QY 1203 GTCAACAGTGTGTGAGTGTACTGTGTGCAAGAGGAGGAGTCCAGTAGAATCT 1262
 DB 1201 GTCAACAGTGTGTGAGTGTACTGTGTGCAAGAGGAGGAGTCCAGTAGAATCT 1260
 QY 1263 CAAGACCTTCCCTCCCTTGAACCTTTCTGAGAGTCTTAAGAGCCAGATTCAT 1322
 DB 1261 CAAGACCTTCCCTCCCTTGAACCTTTCTGAGAGTCTTAAGAGCCAGATTCAT 1320
 QY 1323 CTGCACAAAATAGGTGTGTACTTATAGAGATTGATACAAAGACGATTACAATCT 1382
 DB 1321 CTGCACAAAATAGGTGTGTACTTATAGAGATTGATACAAAGACGATTACAATCT 1380
 QY 1383 CTGAGTGTGCCCCCAAGTACCACTTATGAAGATGCCATGCTTTGTGCAAGATT 1442
 DB 1381 CTGAGTGTGCCCCCAAGTACCACTTATGAAGATGCCATGCTTTGTGCAAGATT 1440
 QY 1443 CTCATGTGAACAGAGGTGTGAGAGAAATGATCAAGCCGTCGACAGATGGCTGC 1502
 DB 1441 CTCATGTGAACAGAGGTGTGAGAGAAATGATCAAGCCGTCGACAGATGGCTGC 1500
 QY 1503 TGTCTCTGTAGCCCAACCATGAGAGCAAGACCTTAAGAGCTTCTCATCCCAAT 1562
 DB 1501 TGTCTCTGTAGCCCAACCATGAGAGCAAGACCTTAAGAGCTTCTCATCCCAAT 1560
 QY 1563 TACAGGAAAAAAGCGTGATGATCTGAAGTTACTATGACCTTCAAAACAGCTTAG 1622
 DB 1561 TACAGGAAAAAAGCGTGATGATCTGAAGTTACTATGACCTTCAAAACAGCTTAG 1620
 QY 1623 TAATTAACCATTTTATACCAATTAATTTTCAATATTAATTAATTAATTAATTAAC 1682
 DB 1621 TAATTAACCATTTTATACCAATTAATTTTCAATATTAATTAATTAATTAATTAAC 1680
 QY 1683 TAACGATGGAACACTTATCACTTCAAAAGCTGTTTATACATAGAAATCAATTAACA 1742
 DB 1681 TAACGATGGAACACTTATCACTTCAAAAGCTGTTTATACATAGAAATCAATTAACA 1740
 QY 1743 GCTTTAATTAAGAACTGTAACTTTGATTAATGCAACATTAAGCAATCTTC 1794

Db 1741 GCTTTAATGAAACTGTACCACTTTGATGATGCAACAATAAGCATCTTC 1792

RESULT 5
AAH99008
ID AAH99008 standard; cDNA, 2161 BP.
XX
XX AAH99008;
XX
XX 12-OCT-2001 (first entry)
XX
XX Human EST-derived coding sequence SEQ ID NO: 865.
DE
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder;
XX biodiversity; gene therapy; nutrition; ss.
OS Homo sapiens.
XX
XX MO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Dzmanac RA, Zhang J, Wehman T;
XX WPI; 2001-476164/51.
XX P-PSDB; AAM24349.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 1; Page 707; 1275bp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
XX
XX Sequence 2161 BP; 639 A; 516 C; 446 G; 560 T; 0 other;

Query Match 97.6%; Score 1783.8; DB 22; Length 2161;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CGGCGATGTCGTCGTCGTGATTAAGCTGCGCGCTGTGACAGAGCGCGTAACCCCGAG 60
Db 3 CGGCGATGTCGTCGTCGTGATTAAGCTGCGCGCTGTGACAGAGCGCGTAACCCCGAG 62
QY 61 AGCGGACGCTGAATGCTGCTGCTGAAACGCGGCATCTCCAGAGGAGTACCAACATG 120
Db 63 AGCGGACGCTGAATGCTGCTGCTGAAACGCGGCATCTCCAGAGGAGTACCAACATG 122
QY 121 ATCTAATCCCGGAGACTTGAGGAGACTCCGAGTAGAACTGTCAACTAGTGTGCAA 180
Db 123 ATCTAATCCCGGAGACTTGAGGAGACTCCGAGTAGAACTGTCAACTAGTGTGCAA 182
QY 181 CAGGGAGCTATTCAATTTTGATGATGATGATGAGTGGTACTCCGGGCGAGATGCCAGATCC 240

Db 183 CAGGGAGCTATTCAATTTTGATGATGATGATGAGTGGTACTCCGGGCGAGATGCCAGATCC 242
QY 241 GCTTGTGAGAGCCCAACAAGATTTGTGACCGGCGAAAAAGCACTTCCAGTCTCAAGCT 300
Db 243 GCTTGTGAGAGCCCAACAAGATTTGTGACCGGCGAAAAAGCACTTCCAGTCTCAAGCT 302
QY 301 GTGTGAGGTGCAATTACACAGAGGCTTCCAGACTGACACAGACCTCTGTGTAAAT 360
Db 303 GTGTGAGGTGCAATTACACAGAGGCTTCCAGACTGACACAGACCTCTGTGTAAAT 362
QY 361 GGACATTTTCCATATATGCTTCCCTGTAGAGCTGAACACATTAATTTTATTTGGGGCC 420
Db 363 GGACATTTTCCATATATGCTTCCCTGTAGAGCTGAACACATTAATTTTATTTGGGGCC 422
QY 421 ATAAATTTCTTAATCAATATGAATGAAGAGGCTTCCAGTCTGTGAATTTCACT 480
Db 423 ATAAATTTCTTAATCAATATGAATGAAGAGGCTTCCAGTCTGTGAATTTCACT 482
QY 481 CACCAAGCTGCTAGACCAACATATGAATATATATATATATATATATATATATATATAT 540
Db 483 CACCAAGCTGCTAGACCAACATATGAATATATATATATATATATATATATATATATAT 542
QY 541 TGTGGATCCGAAACATCACTGCTGTGAAGAAATGAGAGACAGTAAAGTAACTTCA 600
Db 543 TGTGGATCCGAAACATCACTGCTGTGAAGAAATGAGAGACAGTAAAGTAACTTCA 602
QY 601 CAACCACTCCCTGGGAAAAAGATACATGCTCTTATCCAAACAGCACTATCATCGGCT 660
Db 603 CAACCACTCCCTGGGAAAAAGATACATGCTCTTATCCAAACAGCACTATCATCGGCT 662
QY 661 TTTCTCAGGTGTTTGAAGCCACACAGAAAGAAACAAACGGAGCTTCACTGTGATTCAG 720
Db 663 TTTCTCAGGTGTTTGAAGCCACACAGAAAGAAACAAACGGAGCTTCACTGTGATTCAG 722
QY 721 TGACTGGGATATGTAAGGTGCTACGGTGCAGCTGACTGATTCATATTTTCTACTTGTGCA 780
Db 723 TGACTGGGATATGTAAGGTGCTACGGTGCAGCTGACTGATTCATATTTTCTACTTGTGCA 782
QY 781 GGCATGTCATCCGACATTAAGGAACAGTTGTCTGCGCCCAACAAAGAGGCTCCCTTCC 840
Db 783 GGCATGTCATCCGACATTAAGGAACAGTTGTGTCTGCGCCCAACAAAGAGGCTCCCTTCC 842
QY 841 CTCTGATTAACAACAAAGCAAGCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTC 900
Db 843 CTCTGATTAACAACAAAGCAAGCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTC 902
QY 901 TGTGTGCCCATGAGGTGCTGTGTGCGAGGAGTATATTAATGTGAGGCGCAAGAGATCA 960
Db 903 TGTGTGCCCATGAGGTGCTGTGTGCGAGGAGTATATTAATGTGAGGCGCAAGAGATCA 962
QY 961 AGAAGACTTCTTTCTAACAACCACTACTGCGCCCATTAAGGTTCTGTGTTTACC 1020
Db 963 AGAAGACTTCTTTCTAACAACCACTACTGCGCCCATTAAGGTTCTGTGTTTACC 1022
QY 1021 CATCTGAATATATTTTCAATCAACAATTTTGTACTTCACTGAATTTCTTCAAAACAT 1080
Db 1023 CATCTGAATATATTTTCAATCAACAATTTTGTACTTCACTGAATTTCTTCAAAACAT 1082
QY 1081 GCAGAAATGAGGTCACTCTTGAAGAAAGTGCGCAGAAAAAATAGCAGATGCGTCCAG 1140
Db 1083 GCAGAAATGAGGTCACTCTTGAAGAAAGTGCGCAGAAAAAATAGCAGATGCGTCCAG 1142
QY 1141 TGCAATGCTGTCACATAAAGAGGAGGAGCAGACAAAGTGTCTTCTCTTCTTCAATG 1200
Db 1143 TGCAATGCTGTCACATAAAGAGGAGGAGCAGACAAAGTGTCTTCTCTTCTTCAATG 1202
QY 1201 ACCTCAACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1203 ACCTCAACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
QY 1261 CTCAAGACTCTTCTCCCTCTGCTTAACTTTTCTGACATGATCTTAAGAGCCAGATTC 1320
Db 1263 CTCAAGACTCTTCTCCCTCTGCTTAACTTTTCTGACATGATCTTAAGAGCCAGATTC 1322

Oy	361	GGACATTTTCCATATCCGATCTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCC	420
Db	381	GGACATTTTCCATACATCGGCTTCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCC	440
Oy	421	ATTAATTTTCCCTATATGCAAAATATGAATGAAGTGGCCCTTCATGTCTGTGAATTTCACTT	480
Db	441	ATTAATTTTCCCTATATGCAAAATATGAATGAAGTGGCCCTTCATGTCTGTGAATTTCACTT	500
Oy	481	CACCAAGCTGCTGACACACATTAATGAAATTAATAAAAAAGTGTGTCAAGCCGGAAAGCC	540
Db	501	CACCAAGCTGCTGACACACATTAATGAATTAATAAAAAAGTGTGTCAAGCCGGAAAGCC	560
Oy	541	TGTGGGATCCGAACATCATCTGCTTTGTAAAGAAATGAGAGACATGTGAAGTGAATTTCA	600
Db	561	TGTGGGATCCGAACATCATCTGCTTTGTAAAGAAATGAGAGACATGTGAAGTGAATTTCA	620
Oy	601	CAACCACTCCCTCGGGAACAGATACATAGGCTTTATTCACACACAGCACTATCATCGGGT	660
Db	621	CAACCACTCCCTCGGGAACAGATACATAGGCTTTATTCACACACAGCACTATCATCGGGT	680
Oy	661	TTTCTCAGGTGTTGAGCACACACAGAAACAAACGCGAGCTTCAGTGTGTATTTCCAG	720

Qy	1441	TTTCACATGTCACAGCAGCAGGTGTACGACGAGAAAAAGATCACAAGCTTCCACGATGGCT	1500
Db	1461	TTTCACATGTCACAGCAGCAGGTGTACGAGGAAAAAGATCACAAGCTTCCACGATGGCT	1520
Qy	1501	GGTCGCTCTTGTAGCCACCCATGAGAACAGAGCCCTTAAAGGCTTCATGCCACCA	1560
Db	1521	GGTCGCTCTTGTAGCCACCCATGAGAACAGAGCCCTTAAAGGCTTCATGCCACCA	1580
Qy	1561	ATTACAGGAGAAAAACGTGTATGATCCCTGAAGCTTACTATGACGCCATACAAAGAGCTT	1620
Db	1581	ATTACAGGAGAAAAACGTGTATGATCCCTGAAGCTTACTATGACGCCATACAAAGAGCTT	1640
Qy	1621	AGTATATTAACACTTTTATATCCATATAAATTTTCAATATTACTACTAATATGACATTA	1680
Db	1641	AGTATATTAACACTTTTATATCCATATAAATTTTCAATATTACTACTAATATGACATTA	1700
Qy	1681	ACTACGATTTGGAAACTACATTTTCAACTTCAAGCTGTTTTATATCATGAAATCAATTA	1740
Db	1701	ACTACGATTTGGAAACTACATTTTCAACTTCAAGCTGTTTTATATCATGAAATCAATTA	1760
Qy	1741	CAGTTTAAATTTGAAAACGTGAACATTTTGGATATATGCAACATTAAGATCTTC	1794
Db	1761	CAGTTTAAATTTGAAAACGTGAACATTTTGGATATATGCAACATTAAGATCTTC	1814

RESULT 7
AAA75772
ID AAA75772 standard; cDNA; 1918 BP.

AC AAA75772;

DT 22-JAN-2001 (first entry)

DE CDNA encoding a human interleukin 17 receptor-like protein variant.

KW Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;

KW cellular migration; ovulation; neurogenesis; arthritis;

XX

XX

FT	CDS	111..1412
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FT /product= "interleukin 17-receptor-like protein variant"

PN WO200055204-A1.

PD 21-SEP-2000.

PF 06-MAR-2000; 2000WO-US05759.

PR 16-MAR-1999; 99US-0268311.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Shi Y, Ruben SM;

DR WPI; 2000-647065/62.

XX

PT family, and an antagonist and agonist of the polypeptide, useful for

[illegible]

PS Disclosure; Page 237-239; 247pp; English

CC The present sequence encodes a human interleukin 17-receptor-like protein

CC agonists and antagonists. These antagonists and agonists are useful for

CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
 CC cellular migration, ovulation or neurogenesis, such as osteoporosis,
 CC arthritis and autoimmune disorders e.g. systemic lupus erythematosus.
 XX

SQ Sequence 1918 BP; 560 A; 469 C; 426 G; 461 T; 2 other;

Query Match 97.6%; Score 1782.4; DB 21; Length 1918;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1800; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 3 GCGATGCGCTCGTGGATGATGAGCTGGCGCGCTGCGAGGAGCGCGATACCCCGAG 62
 DB 108 GCGATGCGCTCGTGGATGATGAGCTGGCGCGCTGCGAGGAGCGCGATACCCCGAG 167
 QY 63 CCGACGCTTCAATGTGGCTGTGAAGCTGGGCACTCTCCAGATGATGATCAACATGAT 122
 DB 168 CCGACGCTTCAATGTGGCTGTGAAGCTGGGCACTCTCCAGATGATGATCAACATGAT 227
 QY 123 CTATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTCACACTAGTGTGCAACA 182
 DB 228 CTATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTCACACTAGTGTGCAACA 287
 QY 183 GGGGACTATTCATTTTGAATGATGATGAGTGGGTACTCCGGGCAATGCGACATCCG 242
 DB 288 GGGGACTATTCATTTTGAATGATGATGAGTGGGTACTCCGGGCAATGCGACATCCG 347
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 DB 348 TTGTTGAAGGCCCAAGATTTTGTGACGGGCAAAAGCACTTCCAGTCTCAAGCTGT 407
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 DB 408 GTGAGGTGCAATTAACAGAGGCGCTTCAAGCTCAAGCAAGCCCTGTGTGTTAAATGG 467
 QY 363 ACATTTTCCATATTCGCGCTTCCGCTGATGAGTGAACCAAGCTATTTTCAATGGGGCCAT 422
 DB 468 ACATTTTCCATATTCGCGCTTCCGCTGATGAGTGAACCAAGCTATTTTCAATGGGGCCAT 527
 QY 423 AATATTTCTATGCAATATGAAATGAAATGAGTGGCTTCAATGTCTGTGAATTTCACTCA 482
 DB 528 AATATTTCTATGCAATATGAAATGAAATGAGTGGCTTCAATGTCTGTGAATTTCACTCA 587
 QY 483 CCAAGGCTGCTTAAGCAACATTAATGAATATTAATAAAGTGTCAAGGCGGAAAGCTTG 542
 DB 588 CCAAGGCTGCTTAAGCAACATTAATGAATATTAATAAAGTGTCAAGGCGGAAAGCTTG 647
 QY 543 TGGGATCCGGAACATCACTGCTTGTGAAGAAATGAAGAGCACTGAAGTGAATCTTACA 602
 DB 648 TGGGATCCGGAACATCACTGCTTGTGAAGAAATGAAGAGCACTGAAGTGAATCTTACA 707
 QY 603 ACCACTCCCTGGGAAACAGATACATGGCTCTTATCCCAACAGACATATCATCGGGTTT 662
 DB 708 ACCACTCCCTGGGAAACAGATACATGGCTCTTATCCCAACAGACATATCATCGGGTTT 767
 QY 663 TCTCAGGTGTTTGAAGCACAACAGAAAGAAACAAACGCGAGCTTCAAGTGTGATTCAGTG 722
 DB 768 TCTCAGGTGTTTGAAGCACAACAGAAAGAAACAAACGCGAGCTTCAAGTGTGATTCAGTG 827
 QY 723 ACTGGGATAGTGAAGTGTCTACGGTGCAGCTGACTGATCAATATTTTCTACTTGTGGACG 782
 DB 828 ACTGGGATAGTGAAGTGTCTACGGTGCAGCTGACTGATCAATATTTTCTACTTGTGGACG 887
 QY 783 GACTGATCCGATTAAGAAAGAAAGAGTGTCTGTGCCCAAAAGAGGCTCCCTTCCCT 842
 DB 888 GACTGATCCGATTAAGAAAGAAAGAGTGTGTCTGTGCCCAAAAGAGGCTCCCTTCCCT 947
 QY 843 CTGGATTAACAACAAAGAACCGGGAGGCTGCGTGTCTCTCTCTGTCTGTCTGCTG 902
 DB 948 CTGGATTAACAACAAAGAACCGGGAGGCTGCGTGTCTCTCTCTGTCTGTCTGCTG 1007
 QY 903 GTGGCCACATGGGCTGTGTGTGAGAGGATCTATCTAATGTGGAGGACGAAAGATCAAG 962
 DB 1008 GTGGCCACATGGGCTGTGTGTGAGAGGATCTATCTAATGTGGAGGACGAAAGATCAAG 1067

QY 963 AAGACTTCCTTTTCTACCAACACATACGCCCCCATTAAGGTTCTTGGTTTACCA 1022
 DB 1068 AAGACTTCCTTTTCTACCAACACATACGCCCCCATTAAGGTTCTTGGTTTACCA 1127
 QY 1023 TCTGAATATGTTTTCATACACAAATTTGTACTTCACTGATTTTCTTCAAAACCTTGC 1082
 DB 1128 TCTGAATATGTTTTCATACACAAATTTGTACTTCACTGATTTTCTTCAAAACCTTGC 1187
 QY 1083 AGAAGTGAAGTCACTCTTGAAGAGTGGCAGAAAGAAATATGACAGATGGGTCCAGTG 1142
 DB 1188 AGAAGTGAAGTCACTCTTGAAGAGTGGCAGAAAGAAATATGACAGATGGGTCCAGTG 1247
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 DB 1248 CAGTGGCTTGCCACTCAAAAGAGGACGAGCAAAAGTGTCTTCTTTCCAAATGAC 1307
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 DB 1308 GTCAACAGTGTGTGATGTACTGTGTGCAAGAGGAGGAGTCCAGTGAAACTCT 1367
 QY 1263 CAAGACTGTCCCTTGCCTTTAACTTTCTGCAAGTATCTAAGAACCGATTCAT 1322
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 QY 1323 CTGCACAAATTAAGTGTGTCTTATAGAGATTTGATTAACAAAGACGATTACAATGCT 1382
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 QY 1383 CTGAGTGTGTGCCCCCAAGTACCACTTCAAGAGATGCCACTGCTTTTGTGCAAACTT 1442
 DB 1487 CTGAGTGTGTGCCCCCAAGTACCACTTCAAGAGATGCCACTGCTTTTGTGCAAACTT 1546
 QY 1443 CTCATGTCAAGAGAGGTGTCAAGAGGAAAGATCAAGACCTGCCAGATGGCTGC 1502
 DB 1547 CTCATGTCAAGAGAGGTGTCAAGAGGAAAGATCAAGACCTGCCAGATGGCTGC 1606
 QY 1503 TGTCTCTGTAGCCCAACCATGAGAAAGAGACCTTAAAGCTTCTTATCCACCAAT 1562
 DB 1607 TGTCTCTGTAGCCCAACCATGAGAAAGAGACCTTAAAGCTTCTTATCCACCAAT 1666
 QY 1563 TACAGGAAAGAAACGTGTATGATCTGAAAGTTACTATGACGCTTCAAAACGCTTGTG 1622
 DB 1667 TACAGGAAAGAAACGTGTATGATCTGAAAGTTACTATGACGCTTCAAAACGCTTGTG 1726
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 DB 1727 TAATTAAACATTTTATCAATTAATAATTTCAATATTTACTTAATGATGATTAAC 1786
 QY 1683 TAAAGTTGAAACTACATTTTCAACTTCAAGCTGTTTATATACATAGAAATCAATTACA 1742
 DB 1787 TAAAGTTGAAACTACATTTTCAACTTCAAGCTGTTTATATACATAGAAATCAATTACA 1846
 QY 1743 GCTTTAATTGAAACTGTATACATTTTGTATATGCAACATTAAGATTTTCCAAAAAA 1802
 DB 1847 GCTTTAATTGAAACTGTATATCAATTTTGTATATGCAACATTAAGATTTTCAAGCAAAA 1906
 QY 1803 AAAAAAAAAA 1814
 DB 1907 AAAAAAAAAA 1918

RESULT 8
 AA252046
 ID AA252046 strand: cdna; 1918 BP.
 XX
 AC AA252046;
 XX
 DT 09-AUG-2000 (first entry)
 XX
 DE cdna encoding interleukin 17-like receptor protein (IL17RLP)-2.
 XX
 KW Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;

KM resistant chronic infection; acute infection; mycobacterial infection;
 KM T-cell proliferation; IL-2 biosynthesis; lymphocytic leukemia;
 KM T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 KM IL-6 expression; myeloma; plasmacytoma; Lennert's lymphoma;
 KM immunoprotective; cytostatic; hematopoietic; proliferative;
 KM antibacterial; ss.

OS Homo sapiens.

Key Location/Qualifiers
 CDS 111..1412

FT /tag= a
 FT /product= "Interleukin-17 like receptor protein"

PN WO200015759-A1.

PD 23-MAR-2000.

PF 15-SEP-1999; 99WO-US21048.

PR 16-SEP-1998; 98US-0154219.

PR 16-SEP-1998; 98WO-US19121.

PR 16-MAR-1999; 99US-0268311.

PA (HUMA-1) HUMAN GENOME SCI INC.

PI Ruben SM, Shi Y;

DR MPI: 2000-271403/23.

DR P-85DB; AAY70595.

PT Novel polynucleotides encoding interleukin-17-like receptor protein,
 PT useful for diagnosis and treatment of immune system-related disorders,
 PT e.g. sepsis and cancers -

PS Disclosure: Page 141-143; 147pp; English.

XX The patent relates to novel interleukin-17-like receptor
 CC protein (IL-17R). IL-17R is a homologue of the IL-17 receptor and has
 CC a wide range of cytokine receptor-like activities. IL-17R or its
 CC agonists may be used to enhance host defenses against resistant chronic
 CC and acute infections, e.g. mycobacterial infections, via the attraction
 CC and activation of microbicidal leukocytes. It may also be used to
 CC increase T-cell proliferation by stimulating IL-2 biosynthesis, for the
 CC treatment of T-cell mediated autoimmune diseases and lymphocytic
 CC leukaemias. IL-17R may also be used to regulate hematopoiesis and to
 CC treat sepsis. Extracellular IL-17R domains may be used as antagonists
 CC of IL-17R. IL-17R agonists and antagonists can also be used to
 CC modulate IL-6 expression, useful in treatment of cancers such as
 CC myelomas, plasmacytomas and hybridomas and Lennert's lymphoma. The
 CC present cDNA sequence encodes human IL-17R. This cDNA sequence was
 CC derived from sequencing the HAPOR40 cDNA clone (ATCC deposit
 CC number: 209198)

XX Sequence 1918 BP; 560 A; 469 C; 426 G; 461 T; 2 other;

Query Match 97.6%; Score 1782.4; DB 21; Length 1918;

Best Local Similarity 99.3%; Pred. No. 0; Mismatches 11; Indels 1; Gaps 1;

Matches 1800; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 3 GCGATGTCCTGCTGTGTAAGCTGCGCGCTGTGAGAGAGCGCCGATCCCGAGAG 62
 Db 108 GCGATGTCCTGCTGTGTAAGCTGCGCGCTGTGAGAGAGCGCCGATCCCGAGAG 167
 QY 63 CCGACCGTTCATGTCGCTGTAAGCTGCGCGCTGTGAGAGAGCGCCGATCCCGAGAG 122
 Db 168 CCGACCGTTCATGTCGCTGTAAGCTGCGCGCTGTGAGAGAGCGCCGATCCCGAGAG 227
 QY 123 CTAATCCCGAGAGCTTGAGAGAGCTTGAGAGAGCTTGAGAGAGCTTGAGAGAG 182
 Db 228 CTAATCCCGAGAGCTTGAGAGAGCTTGAGAGAGCTTGAGAGAGCTTGAGAGAG 287
 QY 183 GGGGACTATTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 242

Db 288 GGGGACTATTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 347
 QY 243 TTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCCAGCTTCAGCTGT 302
 Db 348 TTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCCAGCTTCAGCTGT 407
 QY 303 GTGAGTGTGCAATTAACAGAGAGCTTCCAGACTCAGACAGACCTCTGTGTAAATG 362
 Db 408 GTGAGTGTGCAATTAACAGAGAGCTTCCAGACTCAGACAGACCTCTGTGTAAATG 467
 QY 363 ACAATTTCTATATGCGCTTCCCTGTGAGAGCTGAAACAAGTCTATTTCAATGGGCGCAT 422
 Db 468 ACAATTTCTATATGCGCTTCCCTGTGAGAGCTGAAACAAGTCTATTTCAATGGGCGCAT 527
 QY 423 AATATTTCTAATGCAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 482
 Db 528 AATATTTCTAATGCAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 587
 QY 483 CCAGGCTGCTAGACCAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 542
 Db 588 CCAGGCTGCTAGACCAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 647
 QY 543 TGGATCCGAACATCATCTGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 602
 Db 648 TGGATCCGAACATCATCTGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 707
 QY 603 ACCACTCCCTGGGAAACAGATATCATCTGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 662
 Db 708 ACCACTCCCTGGGAAACAGATATCATCTGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 767
 QY 663 TCTCAGTGTGTTGAGCCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722
 Db 768 TCTCAGTGTGTTGAGCCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 827
 QY 723 ACTGGGATGTAAG 782
 Db 828 ACTGGGATGTAAG 887
 QY 783 GACTGCATCCGACATTAAG 842
 Db 888 GACTGCATCCGACATTAAG 947
 QY 843 CTGATTAACAACAAAG 902
 Db 948 CTGATTAACAACAAAG 1007
 QY 903 GTGGCAGATGGGTGCTGTGAG 962
 Db 1008 GTGGCAGATGGGTGCTGTGAG 1067
 QY 963 AAGATTCCTTTTTCACACACACACTACTGCCCCCATTAAGTGTGTGTATACCA 1022
 Db 1068 AAGATTCCTTTTTCACACACACACTACTGCCCCCATTAAGTGTGTGTATACCA 1127
 QY 1023 TCTGAATATGTTTTCATCACAATTTGTACTTCACTGAATTTCTCAAAACCATGTC 1082
 Db 1128 TCTGAATATGTTTTCATCACAATTTGTACTTCACTGAATTTCTCAAAACCATGTC 1187
 QY 1083 AGAAGTGAAGTCACTCTTGAAG 1142
 Db 1188 AGAAGTGAAGTCACTCTTGAAG 1247
 QY 1143 CAGTGGCTTGGCACTCAAAAG 1202
 Db 1248 CAGTGGCTTGGCACTCAAAAG 1307
 QY 1203 GTCAACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
 Db 1308 GTCAACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1367
 QY 1263 CAAGACTCTTCCCTTGTGAG 1322

Db	1368	CAGA-CTCTCCCCCTTGCTTAACTTTCTGCAGTGATCTAAGAAGCCAGTTCAT	1426
Qy	1323	CTGCACAAATACGTGTGTGCTCTACTTTAGAGATTGATCAAAAGACATTCACATGCT	1382
Db	1427	CTGCACAAATACGTGTGTGCTCTACTTTAGAGATTGATCAAAAGACATTCACATGCT	1486
Qy	1383	CTCAGTGTCTGCCCCAAGTACCTTCATGAAGATGCCATGCTTCTGTGCACAATT	1442
Db	1487	CTCAGTGTCTGCCCCAAGTACCTTCATGAAGATGCCATGCTTCTGTGCACAACCTT	1546
Qy	1443	CTCCATGTCAAGCAGCAGAGTGTCAAGCAGAAAAAGATCACAAGCCTGCCACGATGGCTGC	1502
Db	1547	CTCCATGTCAAGTACAGTGTGTCAAGCAGAAAAAGATCACAAGCCTGCCACGATGGCTGC	1606
Qy	1503	TGCTCTCTGTGACCCACCCATGAGAGACAAGACCTTAAAGGCTTCTATCCACCAAT	1552
Db	1607	TGCTCTCTGTGACCCACCCATGAGAGACAAGACCTTAAAGGCTTCTATCCACCAAT	1666
Qy	1563	TACAGGAAAAAACGTGTGATGATCCTGGAAGCTTACTATGCAAGCTCAACAACGCTTAG	1622
Db	1667	TACAGGAAAAAACGTGTGATGATCCTGGAAGCTTACTATGCAAGCTCAACAACGCTTAG	1726
Qy	1623	TAAATTAACATTTTATACCAATTAATTTTCAATATTAATTAATTAATGATGACTTAAC	1682
Db	1727	TAAATTAACATTTTATACCAATTAATTTTCAATATTAATTAATTAATGATGACTTAAC	1786
Qy	1683	TAAAGATTGGAACATACATTATTAACAATCTCAAAAGCTTTTATATACATAGAAATCAATTACA	1742
Db	1787	TAAAGATTGGAACATACATTATTAACAATCTCAAAAGCTTTTATATACATAGAAATCAATTACA	1846
Qy	1743	GCTTAATTTGAAAACTGTAAACATTTTGTATATATGCAACAATAAGATCTTCCAAAAAA	1802
Db	1847	GTTTAATTTGAAAACTTAATTAACATTTTGTATATATGCAACAATAAGATCTTCCGCCAAA	1906
Qy	1803	AAAAAAAAAAAAA	1814
Db	1907	AAAAAAAAAAAAA	1918

XX	RESULT 9
XX	AAA75761
ID	AAA75761 standard; cDNA; 1816 BP.
XX	
AC	AAA75761;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	cDNA encoding a human interleukin 17 receptor-like polypeptide.
XX	
KW	Human; interleukin 17-receptor-like protein; IL17R _P ; osteoporosis;
KW	cellular activation; haemostasis; angiogenesis; tumour metastasis;
KW	cellular migration; ovulation; neogenesis; arthritis;
KX	autoimmune disorder; systemic lupus erythematosus; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	10..1280
FT	CDS
FT	/tag= a
FT	/product= "interleukin 17-receptor-like protein"
FT	10..66
FT	/tag= b
FT	67..1287
FT	mat_peptide
FT	/tag= c
XX	
FN	WO20005204-A1.
PD	
PD	21-SEP-2000.
PP	06-MAR-2000; 2000MO-US05759.
PR	
PR	16-MAR-1999; 99US-0268311.
XX	

PA	(HMDA-) HUMAN GENOME SCI INC.
XX	
PI	Shi Y, Ruben SM;
XX	
DR	WPI, 2000-647065/62.
DR	P-Psdb; AAB18750.
XX	
PT	Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system related disorders -
PS	
XX	
CC	Claim 2; Fig 1A-C; 247pp; English.
XX	
CC	The present sequence encodes a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and or preventing disorders related to cellular activation, hemostasis, angiogenesis, tumor metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders e.g. systemic lupus erythematosus.
CC	
SQ	Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
Query Match	97.2%; Score 1775.2; DB 21; Length 1816;
Best Local Similarity	99.1%; Freq. No. 0;
Matches 1795; Conservative	1; Mismatches 14; Indels 2; Gaps 1
OY	3 GGATGTCCTGTGCTCTGATAAGCCTGGCGCGCTGTGCAGAGGCCCTACCCGAGAG 62
DB	7 GCGATGTGCTGTCTGTCTGTAGCCTTGCCGCGCTGTGCAGAGGCCCTACCCGAGAG 66
OY	63 CGACCGTTCAATGTGCTCTGAAACTGGGCCCATCTCCAGACTGATGCTACAATGAT 122
DB	67 CGGACCGTTCAATGTGCTCTGAAACTGGGCCCATCTCCAGAGTGAATGCTACAATGAT 126
OY	123 CTAAATCCCCGAGACTTGAAGGSACTCCGAGTAGAACTCTTACAACACTRAGTGTGCACA 182
DB	127 CTAAATCCCCGAGACTTGAAGGSACTCCGAGTAGAACTCTTACAACACTRAGTGTGCACA 186
OY	183 GGGGCACTATTCAATTTGATGTAAGTGAAGCTGGGTAATCCGGGCGAGTCCGAGCATCCGC 242
DB	187 GGGGCACTATTCAATTTGATGTAAGTGAAGCTGGGTAATCCGGGCGAGTCCGAGCATCCGC 246
OY	243 TTGTTGAAGGCGCACCAAGATTTGTGTGACGGGCAAGAAGCACTTCACGTCTTACAGCTGT 302
DB	247 TTGTTGAAGGCGCACCAAGATTTGTGTGACGGGCAAGAAGCACTTCACGTCTTACAGCTGT 306
OY	303 GTGAGTGCAATTACACACAGAGGCTTCCAGACTCAGACCAGACCTCTGTGTGTAATGG 362
DB	307 GTGAGTGCAATTACACAGAGGCTTCCAGACTCAGACCAGACCTCTGTGTGTAATGG 366
OY	363 ACAATTTCCCTAATGTGGGCTCCCTGTAGAGCTGAACACAGTATTTATATGGGGCCCAT 422
DB	367 ACAATTTCCCTAATGTGGGCTCCCTGTAGAGCTGAACACAGTATTTATATGGGGCCCAT 426
OY	423 AATATTTCCCTAATGTGAATATGTAAGATGGCCCTTCATGTCTGTGAATTTCACTCA 482
DB	427 AATATTTCCCTAATGTGAATATGTAAGATGGCCCTTCATGTCTGTGAATTTCACTCA 486
OY	483 CCAGGCTGCTAGACACACATATATGAATATATAAAAAGTGTGTCAAGGCCGGAAGCTTG 542
DB	487 CCAGGCTGCTAGACACACATATATGAATATATAAAAAGTGTGTCAAGGCCGGAAGCTTG 546
OY	543 TGGGATCCGAACATCACTGCTTTGTAAGAAATGAGAGACAGTAGAAGTGAACCTTACA 602
DB	547 TGGGATCCGAACATCACTGCTTTGTAAGAAATGAGAGACAGTAGAAGTGAACCTTACA 606
OY	603 ACCACTCCCTGGGAAAAGAGATACCTGGCTTTATCCCAACAGACATATATCCGGGTTT 662
DB	607 ACCACTCCCTGGGAAAAGAGATACCTGGCTTTATCCCAACAGACATATATCCGGGTTT 666
OY	663 TCCTACGAGTGTGAGCCACACAGAGAAAACAAACGACAGCTTCAGTGTGATTCAGTG 722

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Db 667 TCTCAGGTGTTTACGACACCCAGAAAGAAACAAACCGAGCTTCAGTGGATTCACAGT 726
Qy 723 ACTGGGATAGTAAGGTGTACGTGACGTACTCATATTTCTCTACTTGGCAGC 782
Db 727 ACTGGGATAGTAAGGTGTACGTGACGTACTCATATTTCTCTACTTGGCAGC 786
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Db 787 GACTGATCCGACATTAAGGAACAGTTGTCTGTGCCCAACAAACAGGCGTCCCTTCCCT 846
Qy 843 CTGGATTAACAAACAAAGCAAGCCGGAGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCT 902
Db 847 CTGGATTAACAAACAAAGCAAGCCGGAGGTGGCTGTCTCTCTCTCTCTCTCTCTCTCT 906
Qy 903 GTGGCCACATGGGTGTGGGTGGGAGGATCTATCTAATGTGGAGGACGAAAGATCAAG 962
Db 907 GTGGCCACATGGGTGTGGGTGGGAGGATCTATCTAATGTGGAGGACGAAAGATCAAG 966
Qy 963 AAGACTTCTTTTCTACACACACACTACTGCCCCCATTAAGGTTCTGTGTTCACCA 1022
Db 967 AAGACTTCTTTTCTACACACACACTACTGCCCCCATTAAGGTTCTGTGTTCACCA 1026
Qy 1023 TCTGAATATGTTTCAATCAACAAATTTGTTACTTCACTGAATTTCTTCAAAACATTCG 1082
Db 1027 TCTGAATATGTTTCAATCAACAAATTTGTTACTTCACTGAATTTCTTCAAAACATTCG 1086
Qy 1083 AAGAGAGGTCTATCTTGAAGAGGAGAAAGAAAGAAATGACAGATGGTCCAGT 1142
Db 1087 AAGAGAGGTCTATCTTGAAGAGGAGAAAGAAAGAAATGACAGATGGTCCAGT 1146
Qy 1143 CAGTGTCTTCCACTCAACAAAGAGGACGACAAAGTGTCTTCTCTTCTTCTTCAATGAC 1202
Db 1147 CAGTGTCTTCCACTCAACAAAGAGGACGACAAAGTGTCTTCTCTTCTTCTTCAATGAC 1206
Qy 1203 GTCAACAGTGTGTGCAATGTGTACTGTGGCAGAGGAGGAGTCCAGTGAATCTT 1262
Db 1207 GTCAACAGTGTGTGCAATGTGTACTGTGGCAGAGGAGGAGTCCAGTGAATCTT 1266
Qy 1263 CAAGACTCTTCCCTTCCCTTGAACCTTCTTCTGAGAGATTAAGAGCCAGATTCAT 1322
Db 1267 CAAGAC-TCTTCTCTTCTTGAACCTTCTTCTGAGAGATTAAGAGCCAGATTCAT 1324
Qy 1323 CTGCACAAATAGCTGTGTCTTCTTGAAGATTAAGAGATTAAGATTCATGCT 1382
Db 1325 CTGCACAAATAGCTGTGTCTTCTTGAAGATTAAGAGATTAAGATTCATGCT 1384
Qy 1383 CTGAGTGTCTGCCCAAGTACCACTTCATGAAGATGCACTGTCTTCTGTGCAAACTT 1442
Db 1385 CTGAGTGTCTGCCCAAGTACCACTTCATGAAGATGCACTGTCTTCTGTGCAAACTT 1444
Qy 1443 CTTCATGTCAAGAGGAGGTGTGAGAGAGAAAGATCAACAGCCGCAACGATGCTGC 1502
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Qy 1803 AAAAAAAAAAAAA 1814
Db 1805 AAAAAAAAAAAAA 1816

RESULT 10
AAZ52035
ID AAZ52035 standard; cDNA; 1816 BP.
XX
XX AAZ52035;
XX
XX 09-AUG-2000 (first entry)
XX
XX
XX cDNA encoding interleukin 17-like receptor protein (IL17RLP)-1.
XX
XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
XX resistant chronic infection; acute infection; mycobacterial infection;
XX T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
XX IL-6 expression; myeloma; plasmacytoma; Lemmer's lymphoma;
XX Immunoprotective; cytostatic; hematopoietic; proliferative;
XX antibacterial; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 10..1290
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XX FT /*tag= c
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XX FT /note= "This corresponds to an alternative leader
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XX FT 67..1287
XX FT /*tag= d
XX FT /product= "Mature IL17RLP"
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XX FT /note= "This is an alternative mature protein
XX as described on Page 3 of the specification"
XX
XX WO200015759-A1.
XX
XX 23-MAR-2000.
XX
XX 15-SEP-1999; 99WO-US21048.
XX
XX 16-SEP-1998; 98US-0154219.
XX 16-SEP-1998; 98WO-US19121.
XX 16-MAR-1999; 99US-0268311.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Shi Y,
XX PI
XX
XX MPI, 2000-271403/23.
XX
XX P-P8DB; AAY70591.
XX
XX Novel polynucleotides encoding interleukin-17-like receptor protein,
XX useful for diagnosis and treatment of immune system-related disorders,
XX e.g. sepsis and cancers -
XX
XX Claim 2; Fig 1; 147bp; English.
XX
XX The patent relates to novel interleukin-17-like receptor
XX protein (IL-17RLP). IL-17RLP is a homologue of the IL-17 receptor and has

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AA235746
ID AA235746 standard; cDNA; 1816 BP.
AC AA235746;
XX
XX
DT 01-FEB-2000 (first entry)
XX
DE Human interleukin 17 receptor like protein encoding cDNA.
XX
XX Human; interleukin 17 receptor like protein; IL17RP; IL-17;
XX diagnosis; detection; immune system related disorder; haemostasis;
XX cellular activation; angiogenesis; tumour metastasis; ovulation;
XX cellular migration; neurogenesis; infection; T-cell proliferation;
XX autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
XX sepsis; tumour; cancer; interstitial lung disease; arthritis;
XX lymphoma; immunosuppression; immunity; inflammatory bowel disease;
XX myelo suppression; SR.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 10..1290
FT /tag= a
FT /product= "interleukin 17 receptor like protein"
FT sig_peptide 10..66
FT /tag= b
FT mat_peptide 67..1287
FT /tag= c
XX
XX MO9914240-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-US19121.
XX
XX 17-SEP-1997; 97US-0059133.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Shl Y, Ruben SM;
PI
XX
XX WPI: 2000-061918/05.
DR
XX
XX P-PSDB; AAY49946.
DR
XX
XX New human interleukin-17 receptor like protein, e.g. to treat disorders
XX relating to cellular activation -
XX
XX
XX Claim 2; Fig 1; 133pp; English.
XX
XX The present sequence encodes human interleukin 17 receptor like protein
XX (IL17RP), isolated from a cDNA library of human adult pulmonary tissue.
XX IL17RP and its agonists can be used to treat disorders relating to
XX cellular activation, haemostasis, angiogenesis, tumour metastasis,
XX cellular migration and ovulation, and neurogenesis. They can also be
XX used to enhance host defences against resistant chronic and acute
XX infections, e.g. mycobacterial infections via the attraction and
XX activation of microbial leukocytes. IL17RP may also be used to increase
XX T-cell proliferation by the stimulation of IL-2 biosynthesis for the
XX treatment of T-cell mediated autoimmune diseases and lymphocytic
XX leukaemia, to regulate haematopoiesis by regulating the activation and
XX differentiation of various haematopoietic progenitor cells, e.g. to
XX release mature leukocytes from the bone marrow following chemotherapy,
XX i.e. in stem cell mobilisation or to treat sepsis. The products can also
XX be used for the diagnosis or treatment of immune system related disorders
XX e.g. tumours, cancers, interstitial lung disease, and any dysregulation
XX of immune cell function including autoimmunity, arthritis, leukaemias,
XX lymphomas, immunosuppression, immunity, humoral immunity, inflammatory
XX bowel disease, or myelo suppression.
XX
XX Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
XX
XX Query Match 97.2%; Score 1775.2; DB 21; Length 1816;
XX
XX Best Local Similarity 99.1%; Pred. No. 0;

Matches 1795; Conservative 1; Mismatches 14; Indels 2; Gaps 1;
QY 3 GCGATGTCGCTGCTGTGATTAAGCCTGCGCGCTGTGAGAGCGCCCTCCAGAG 62
DB 7 GCGATGTCGCTGCTGTGATTAAGCCTGCGCGCTGTGAGAGCGCCCTCCAGAG 66
QY 63 CCGACCGTTCAATGTGCTCTGAAACTGGGCCATCTCCAGAGTGTGCTTACAACATGAT 122
DB 67 CCGACCGTTCAATGTGCTCTGAAACTGGGCCATCTCCAGAGTGTGCTTACAACATGAT 126
QY 122 CTAATCCCGGAGCTTGAAGGAGCCTCCGAGTAAGAACCTGTACAACCTGTGTGGAACA 182
DB 127 CTAATCCCGGAGCTTGAAGGAGCCTCCGAGTAAGAACCTGTACAACCTGTGTGGAACA 186
QY 183 GGGGACTATTCATTTTGTATGATGAATGAAGCTGGGTAAGTCCGGGAGATCCGACATCCGC 242
DB 187 GGGGACTATTCATTTTGTATGATGAATGAAGCTGGGTAAGTCCGGGAGATCCGACATCCGC 246
QY 243 TTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCACAGCTGT 302
DB 247 TTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCACAGCTGT 306
QY 303 GTGAGGTGCAATTAACACAGAGGCTTCCAGACTCAGACCAACCTCTGTGTGTAATG 362
DB 307 GTGAGGTGCAATTAACACAGAGGCTTCCAGACTCAGACCAACCTCTGTGTGTAATG 366
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DB 367 ACATTTTCTATATGCGCTCCCTGTAGAGCTGAACACAGTCTATTTCTATGGGGCCCAT 426
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QY 483 CCAAGGCTGCTTAGACCAACATTAATGAATTAATAAATAAATGTGTCAAGGCCGGAAGCCTG 542
DB 487 CCAAGGCTGCTTAGACCAACATTAATGAATTAATAAATAAATGTGTCAAGGCCGGAAGCCTG 546
QY 543 TGGGATCCGAACATCACTGCTGTGAAGAAATGAGAGACAGTGAAGTGAATTCACCA 602
DB 547 TGGGATCCGAACATCACTGCTGTGAAGAAATGAGAGACAGTGAAGTGAATTCACCA 606
QY 603 ACCACTCCCTGGGAAACAGATATACATGCTCTTATCCAACACAGACATATCATCGGGTTT 662
DB 607 ACCACTCCCTGGGAAACAGATATACATGCTCTTATCCAACACAGACATATCATCGGGTTT 666
QY 663 TCTCAGTGTGTTGAGCCACACACCAAGAAACAAACGCGAGCTTCAGTGTGATTCAGTGTG 722
DB 667 TCTCAGTGTGTTGAGCCACACCAAGAAACAAACGCGAGCTTCAGTGTGATTCAGTGTG 726
QY 723 ACTGGGATGAGAAAGTGCTACCGGTGAGCTGACTGCATATTTCTACTTGTGGCAGC 782
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DB 1027 TCTGAATATGTTTTCATCAACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTCG 1086

QY 181 CAGGGACATATTCATTTTGATGATGTAAGTGGTACTCCGGGCGAGATGCCAGATCC 240
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 QY 336 ----- 335
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 Db 825 CTTCCCTGGGAAACAGATATCATGCTTTATCCACACAGCACTATCATGCGGTTTTCTC 884
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 Db 885 AGGTGTTGAGCCACACGAGAGAAACAAACGAGCTTCAGTGGGATTTCCAGTACTG 944
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 Db 1185 CTTCTCTTTCTACACACACACTACTGCCCCCATTAAGGTTCTTGTGTTTACCATCTG 1244
 QY 1027 AATAATGTTTCATCACAACAATTTGTTACTTCACTGAATTTCTTCAAAACGATGAGAGA 1086
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 QY 1087 GTAGAGTATCTCTTGAAGAAAGTGGCAGAAAAAGAAAAATAGCAGATGGTCCAGTCACT 1146

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 Db 1425 ACAGTGTGCGATGATGATACCTGTGCGAAGAGGAGGCGAGTCCAGTGAACCTCTCAAG 1484
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 Db 1545 ACAAAATAGTGTGCTACTTATAGAGATGATTAACAAAACAGATTCAATGCTCTCA 1604
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 Db 1605 GTGTGCGCCCAAGTACACATTCATGAAGATGCCAGTCTTCTGTGAGAACTTCTCC 1664
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 Db 1845 TAAACATTTTATACCAATTAATAATTTTCAATATTAATTAATGATGATTAATTAAC 1904
 QY 1687 GATTGGAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1746
 Db 1905 GATTGGAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1964
 QY 1747 TAATTGAAAACCTGAACATTTTGTATTAATGCAACATAAAGATCTTC 1794
 Db 1965 TAATTGAAAACCTGAACATTTTGTATTAATGCAACATAAAGATCTTC 2012

RESULT 13
 ABA03201
 ID ABA03201 standard; cDNA; 2015 BP.
 XX
 AC ABA03201;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Human IL-17 receptor like protein #2 coding sequence.
 XX
 KW Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
 KW antiproliferative; antimicrobial; anorectic; nootropic; neuroprotective;
 KW antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy;
 KW interleukin 17; immune system disorder; infection; weight; reproductive;
 KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
 KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
 KW tumour; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT /-tag= a
 FT /product= "Human IL-17 receptor-like protein #2"
 XX

PN WO200168705-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 16-MAR-2001; 2001MO-US08688.
 XX
 PR 16-MAR-2000; 2000US-189923P.
 PR 12-MAY-2000; 2000US-204208P.
 PR 27-NOV-2000; 2000US-0723232.
 PR 02-FEB-2001; 2001US-266159P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;
 DR WPI; 2002-055100/07.
 DR P-PSDB; AAM47458.
 XX
 PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
 PT polypeptides, useful for treating, diagnosing, ameliorating or
 PT preventing immune system disorders (e.g. psoriatic arthritis) and
 PT infections (e.g. viral infections) -
 PS Claim 1; Fig 3; 239pp; English.
 XX
 CC The present invention relates to novel human nucleic acids encoding
 CC interleukin 17 (IL-17) receptor like proteins. The present sequence is
 CC one such coding sequence. The IL-17 receptor-like proteins and coding
 CC sequences are useful for treating a pathological condition related to
 CC immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
 CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction
 CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
 CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
 CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.
 CC ischaemia), eye disorders, reproductive disorders, tumours and
 CC inflammation.
 XX
 SQ Sequence 2015 BP; 541 A; 499 C; 475 G; 500 T; 0 other;
 Query Match 85.0%; Score 1552.4; DB 24; Length 2015;
 Best Local Similarity 89.3%; Pred. No. 0;
 Matches 1758; Conservative 0; Mismatches 36; Indels 174; Gaps 1;

Db 465 CCGTGCTAAATTTTGTAGTTTTTTGAGAGGGGTTTCAACCGTGTGCTGTGTAATT 524
 Qy 336 -----CAGCCAGACCCCTCTGTGGTAAATGACAT 366
 Db 525 CCAAGTCTCAGGCGATCTGCTGCTCGGCTTCCAAAGTGTGGATTAAGATGACAT 584
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 Db 645 TTTCCTAATCGAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACTCACAG 704
 Qy 487 GCTGCTTAGACCACTAATATGAATATATAAATAAAGTGTCAAGGCGGAGGCTGTGG 546
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 Db 765 ATCCGAACATCACTGCTTGTAAAGAAATGAGAGACAGTAAAGTAACTTCAACCA 824
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 Db 825 CTCCCTTGGGAAAACATATATAGTCTTTATCCACACAGCACTATCCGGGTTTTC 884
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 Db 1545 ACAATATGTTGTGTCTACTTTAGAGAGATTGATCAAAAGACATTAATGCTCTGA 1604


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Qy 721 TGACTGGGATAGTAGAGGTGCTACGGGTGACGTGACTGCATATTTTCTACTTTGGCA 780
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Qy 841 CTCTGATTAACAACAAAGAACGCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTG 900
Db 729 CTCTGATTAACAACAAAGAACGCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTG 788
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Qy 1201 ACCTCAACAGTGTGTGCGATGTACCTGTGGCAAGACGAGGAGTCCGAGTGAAGACT 1260
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Db 1209 ATCTGACAAATACGTGTGTGTCTACTTTAGAGATTTGATACAAAGAGATTAACAATG 1268
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Qy 1801 AAAAAAAAAAAAAA 1813

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Db 1689 AAAAAAAAAAAAAA 1701
RESULT 15
AAE64039
ID AAE64039 standard; cDNA; 1701 BP.
XX
XX AAE64039;
AC
XX
XX 05-APR-2001 (first entry)
DT
XX
XX cDNA encoding human secreted protein #40.
DE
XX
XX Secreted protein; prevention; treatment; diagnosis; disease;
KM infection; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200100806-A2.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 21-JUN-2000; 2000MO-IB00951.
PF
XX
XX 25-JUN-1999; 99US-0141032.
PR
XX 21-DEC-1999; 99US-0469099.
XX
XX
XX (BEST ) GENSET.
PA
XX
XX Dumas Milne Edwards J, Bouquelere L, Jobert S;
PI
XX
XX WPI; 2001-071487/08.
DR
XX
XX
XX
XX
XX 49 Secreted proteins and the nucleic acids encoding them, useful in
PT gene therapy and for detecting similar sequences in samples -
XX
XX
XX Claim 1; Page 259-261; 307pp; English.
PS
XX
XX The present invention relates to 49 Secreted proteins and the cDNAs
CC encoding them. The protein and nucleic acids may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate protein expression.
XX
XX
XX Sequence 1701 BP; 499 A; 412 C; 372 G; 418 T; 0 other;
SQ
Query Match 83.6%; Score 1527.8; DB 22; Length 1701;
Best Local Similarity 92.3%; Pred. No. 0; Mismatches 12; Indels 128; Gaps 1;
Matches 1673; Conservative 0;
Qy 1 CCGCGATGTGCGTCTGATTAAGCTTGCGCGCTGTGACAGAGCGCGTACCCCGAG 60
Db 17 CCGCGATGTGCGTCTGATTAAGCTTGCGCGCTGTGACAGAGCGCGTACCCCGAG 76
Qy 61 AGCCGACCGTTCAATGTGCTGTGAAGCTGGGCACTTCCAGAGTGAATGATCAACATG 120
Db 77 AGCCGACCGTTCAATGTGCTGTGAAGCTGGGCACTTCCAGAGTGAATGATCAACATG 136
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Db 137 ATCTAATCCCGGAGACTTGAGGAGACTCCGAGTGAAGAGCTGTGTCAACTAGTGTGCA 196
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Db 197 CAGGGACATTAATTTGATGAATGTAAGGTGGGTACTCCGGGACAGTGCACATCC 247
Qy 241 GCTTTGGAAGGCCAACAGATTTGTGAGCGGCAAAAGCAACTTCCAGTCTTACAGCT 300
Db 248 ----- 247
Qy 301 GTGTAGGTGCAATTAACACAGAGGCTTCCAGACTCAGACAGAGACCTCTGTGTGAAT 360
Db 248 -----T 248

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QY 361 GGACATTTTCTATATGCGCTTCCCTGTAGAGCTGAACACAGCTCTTTTCATTTGGGGCCC 420
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DB 309 ATATATTTCTTAAATGCAAAATATGAATGAAGATGGCCCTTCATGTCTGTGAATTCACCT 368
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DEFINITION Sequence 1 from Patent WO0168705.
ACCESSION AX253204
VERSION AX253204.1 GI:15986346
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REFERENCE 1 (bases 1 to 1841)
AUTHORS Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S. and
Nguyen, H.Q.
TITLE Il-17 receptor like molecules and uses thereof
JOURNAL Patent: WO 0168705-A 1 20-SEP-2001;
Amgen Inc. (US)
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Best Local Similarity 99.7%; Pred. No. 0;
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DEFINITION Sequence 17 from Patent WO0208285.
ACCESSION AX365258
VERSION AX365258.1 GI:18697003
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ORGANISM Homo sapiens
REFERENCE 1 Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS		Gorman, D.M.	
TITLE		Mammalian receptor proteins; related reagents and methods	
JOURNAL		Patent: WO 0190358-A 1 29-NOV-2001;	
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REFERENCE 1 (bases 1 to 2042)
 Strausberg, R.
 Direct Submission
 Submitted (16-NOV-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villalon@bcm.tmc.edu
 Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
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Clone distribution: MGC clone distribution information can be found
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AUTHORS Shi,Y., Ullrich,S.J., Zhang,J., Connolly,K., Grzegorzewski,K.J.,
Barber,M.C., Wang,W., Wathen,K., Hodge,V., Fisher,C.L., Olsen,H.,
Ruben,S.M., Knyazev,I., Cho,Y.H., Kao,V., Wilkinson,K.A.,
Carrell,J.A. and Ebner,R.
TITLE A novel cytokine receptor-ligand pair. Identification, molecular
characterization, and in vivo immunomodulatory activity
J. Biol. Chem. 275 (25), 19167-19176 (2000)
MEDLINE 20317118
PUBMED 10749887
REFERENCE 2 (bases 1 to 1816)
AUTHORS Shi,Y.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1999) Molecular Biology, Human Genome Sciences,
Inc., 9410 Key West Avenue, Rockville, MD 20850, USA
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AUTHORS		Zhang, W. and Cao, X.	
TITLE		Direct Submission	
JOURNAL		Submitted (29-MAR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R. China	
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RESULT 9

AX253207

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

AX253207

Sequence 4 from Patent WO0168705.

AX253207

AX253207.1

GI:15986348

2015 bp

DNA

linear

PAT 05-OCT-2001

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LOCUS	AX061651
DEFINITION	Sequence 56 from Patent WO0100806.
ACCESSION	AX061651
VERSION	AX061651.1 GI:12406761
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SOURCE	human.
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1701)
TITLE	dumas milne Edwards,J.B., Bougueleret,L. and Jobert,S. Complementary dna's encoding proteins with signal peptides
JOURNAL	Patent: WO 0100806-A 56 04-JAN-2001;
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DEFINITION Sequence 6 from Patent WO0168705.
ACCESSION AX253209
VERSION AX253209.1 GI:15986350
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
Nguyen,H.Q.
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JOURNAL Patent: WO 0168705-A 6 20-SEP-2001;
Amgen Inc. (US)
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DEFINITION Sequence 157 from Patent WO0116318.
ACCESSION AX092426
VERSION AX092426.1 GI:13444527
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1515)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godoski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 157 08-MAR-2001;
Genentech, Inc. (US)
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Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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ACCESSION AX376332
VERSION AX376332.1 GI:19170557
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Chen, J., Deanoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 399 20-SEP-2001;
Genentech, Inc. (US)
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Location/Qualifiers
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BASE COUNT 404 a 384 c 363 g 364 t
ORIGIN
Query Match 82.6%; Score 1509.2; DB 6; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Search completed: May 28, 2003, 06:38:21
Job time : 4683.37 secs

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ALIGNMENTS

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ACCESSION
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VERSION
AL565993.1 GI:12917920
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1.
REFERENCE
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
Contact: Genoscope
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequ@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 657)
Normalizaton and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Forward
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 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
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 was created for the program, Gene Discovery in the Visual
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VERSION BE539514.1 GI:9768159
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 641)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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BASE COUNT 206 a 152 c 118 g 165 t
ORIGIN

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DB 301 CAGCAGGTGTACGACGAGAAAGATCAAGCTGCGACAGTGGCTGTGCTCTTGTAG 360
QY 2544 CCCACCCATGAGAGCAAGAGACCTTAAAGGCTTCTATCCCACTTACAGGGGAAAA 2603
DB 361 CCCACCCATGAGAGCAAGAGACCTTAAAGGCTTCTATCCCACTTACAGGGGAAAA 420
QY 2604 AGCTGTGATGATCCTGAAGCTTACTATGAGCGCTACAAACAGCTTGTAGTAATTAACAT 2663
DB 421 AGCTGTGATGATCCTGAAGCTTACTATGAGCGCTACAAACAGCTTGTAGTAATTAACAT 480
QY 2664 TTTATACCAATAAAATTTTCAATATTAATACTAATATGAGCAATTAACAGATTGAA 2723
DB 481 TTTATACCAATAAAATTTTCAATATTAATACTAATATGAGCAATTAACAGATTGAA 539
QY 2724 ACTACATTTACACTTCAAGCTGTTTTATACATAGAAATCAATTAACAGTTTAAATGAA 2783
DB 540 ACTACATTTACACTTCAAGCTGTTTTATACATAGAAATCAATTAACAGTTTAAATGAA 599
QY 2784 AACTGTAAACATTTTGAATGATCAACAAATAAAGCATCTTC 2823
DB 600 AACTGTAAACATTTTGAATGATCAACAAATAAAGCATCTTC 639

RESULT 6
BI823321
LOCUS 603041231F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182255 5',
DEFINITION mRNA sequence.
ACCESSION BI823321
VERSION BI823321.1 GI:15934871
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 946)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11454 row: m column: 08
High quality sequence stop: 795.

FEATURES

Location/Qualifiers
1..946
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182255"
/lab_host="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
BASE COUNT 240 a 239 c 243 g 224 t
ORIGIN

Query Match 21.7%; Score 619.6; DB 13; Length 946;
Best Local Similarity 92.9%; Pred. No. 4.4e-103;
Matches 702; Conservative 0; Mismatches 4; Indels 50; Gaps 3;

QY 2 GCGATGTGCTGCTGCTGATGAAGCTGCGCGCTGTCCAGAGCGCGTACCCGAGA 61
DB 1 GCGATGTGCTGCTGCTGCTGATGAAGCTGCGCGCTGTCCAGAGCGCGTACCCGAGA 60
QY 62 GCGAGCCGTTCAATGTGGCTCTGAAACTGGGCACTCTCCAGAGTGGATGCTACAATGA 121
DB 61 GCGAGCCGTTCAATGTGGCTCTGAAACTGGGCACTCTCCAGAGTGGATGCTACAATGA 120
QY 122 TCTAATCCCGGAGACTTGAAGGACCTCGAGTAGAACTGTGTACAACTAGTGTGCAAC 181
DB 121 TCTAATCCCGGAGACTTGAAGGACCTCGAGTAGAACTGTGTACAACTAGTGTGCAAC 180
QY 182 AGGGACTATTCAATTTGATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGATCCG 241
DB 181 AGGGACTATTCAATTTGATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGATCCG 240
QY 242 CTGTGTGAAGGCCCAACAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTCAGCTG 301
DB 241 CTGTGTGAAGGCCCAACAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTCAGCTG 300
QY 302 TGTGAGGTGCAATTAACAGAGGCTTCCAGACTCAGACCAGACCTCTGTGTGTAATG 361
DB 301 TGTGAGGTGCAATTAACAGAGGCTTCCAGACTCAGACCAGACCTCTGTGTGTAATG 360
QY 362 GACATTTTCTATATCGGCTCCCTGTAGAGCTGAACACAGTCTATTTCAATGGGGCCA 421
DB 361 GACATTTTCTATATCGGCTCCCTGTAGAGCTGAACACAGTCTATTTCAATGGGGCCA 420
QY 422 TAATATTCCTAATCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTTCACTC 481
DB 421 TAATATTCCTAATCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTTCACTC 480
QY 482 ACCAGGCTGCTAGACCAATTAATAATAAATAAAGTGTGTCAAGGCCGCGAAGCT 541
DB 481 ACCA-----GGAAGCCT 492
QY 542 GTGGATCGAATCATCACTGCTTTGAAG-AAGAATGAGGAGACAGTAGAAGTGAATTC 600
DB 493 GTGGATCGAATCATCACTGCTTTGAAGAAAGATGAGGAGACAGTAGAAGTGAATTC 552
QY 601 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACACAGCACTATCATCGGT 660
DB 553 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACACAGCACTATCATCGGT- 611
QY 661 TTTCTCAGGTGTTGAGCCACACCAAGAAACAAACGCGAGCTTTCAGTGTGTGATTCCAG 720

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Db 612 TTTCTCAGGTGTTTGAGCCACACGAGAAACAAACGCGAGCTTCAGTGGTGAATCCAG 671
Qy 721 TGAAGTGGGATAGTGAAGGTGCTACGGTGCAGGTAA 756
Db 672 TGAAGTGGGATAGTGAAGGTGCTACGGTGCAGCTGA 707

RESULT 7
BG433769/c
LOCUS BG433769 630 bp mRNA linear EST 14-MAR-2001
DEFINITION 602497744F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4611491 5',
mRNA sequence.
ACCESSION BG433769
VERSION BG433769.1 GI:13340275
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 630)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1358 row: g column: 12
High quality sequence stop: 610.
Location/Qualifiers
1. .630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4611491"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcgattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCG-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGGCCGACATG-dt(30)EN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 170 a 111 c 149 g 200 t
ORIGIN
source
Query Match 20.9%; Score 598.2; DB 12; Length 630;
Best Local Similarity 97.9%; Pred. No. 4e-99;
Matches 606; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2214 TTCTCTTTTCCAAATGACGTCAACAGTGTGTGGATGGTGTGGCGAAGAGCGAGGCG 2273
Db 626 TCCTCTTTTCCAAATGACGTCAACAGTGTGTGGATGGTGTGGCGAAGAGCGAGGCG 567
Qy 2274 AGTCCAGTGAAGACTCTCAAGACCTCTTCCCTTGCCTTTAACTTTCTGCGAGTGT 2333
Db 566 AGTCCAGTGAAGACTCTCAAGACCTCTTCCCTTGCCTTTAACTTTCTGCGAGTGT 507
Qy 2334 CTAAGAAGCCAGATTCATCTGCACAATACGTGGTGGTGTCTACTTTAGAGAGATTGATACA 2393
Db 506 CTAAGAAGCCAGATTCATCTGCACAATACGTGGTGGTGTCTACTTTAGAGAGATTGATACA 447
Qy 2394 AAAGAGATTAAATGCTCTCAGTGTCTGCCCAAGTACACTTCATGAAAGATGCCACT 2453

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Db 446 AAAGAGATTAAATGCTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGATGCCACT 387
Qy 2454 GCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCTCAGCAGGAAAAAGATCACAA 2513
Db 386 GCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCTCAGCAGGAAAAAGATCACAA 327
Qy 2514 GCCTGCCAGATGGTGTCTCTCTTGTAGCCACCCATGAGAAGCAAGAGACCTTTAAAG 2573
Db 326 GCCTGCCAGATGGTGTCTCTCTTGTAGCCACCCATGAGAAGCAAGAGACCTTTAAAG 267
Qy 2574 GCTTCTTATCCCACTTACAGGGAAGAAACGCTGTGATGATCCTGAAAGCTTACTATGCA 2633
Db 266 GCTTCTTATCCCACTTACAGGGAAGAAACGCTGTGATGATCCTGAAAGCTTACTATGCA 207
Qy 2634 GCCTCAAAACAGCCTTAGTAATTAATAAACAATTTATACCAATAAAATTTTCAATATTACT 2693
Db 206 GCCTCAAAACAGCCTTAGTAATTAATAAACAATTTATACCAATAAAATTTTCAATATTACT 147
Qy 2694 AACTAATGATGATTAACCTAAGATTTGGAACCTAATTTTCAAACTTTCAAAAGCTGTTTTAT 2753
Db 146 AACTAATGATGATTAACCTAAGATTTGGAACCTAATTTTCAAACTTTCAAAAGCTGTTTTAT 87
Qy 2754 ACATAGAATCAATTAACAGCTTTAATGAAACTGTAACCAATTTGATTAATGCAACAATA 2813
Db 86 ACATAGAATCAATTAACAGCTTTAATGAAACTGTAACCAATTTGATTAATGCAACAATA 27
Qy 2814 AAGCATCTTCCAAAAA 2832
Db 26 AAGCATCTTCCAAAAA 8

RESULT 8
LOCUS AW970151 680 bp mRNA linear EST 01-JUN-2000
DEFINITION EST382232 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.
ACCESSION AW970151
VERSION AW970151.1 GI:8159996
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 680)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt,
I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeaman, T. J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 273
Seq primer: Forward
Location/Qualifiers
1. .680
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGK"
/note="Vector: pBluescriptSKm"
BASE COUNT 209 a 162 c 134 g 174 t 1 others
ORIGIN
source
Query Match 20.5%; Score 585; DB 10; Length 680;
Best Local Similarity 96.9%; Pred. No. 9.9e-97;
Matches 628; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

Qy 2053 CTGAATATGTTTCCATCACACAATTTGTTACTTCTCAGTGAATTTCTTCAAAACCATTTGCA 2112
Db 1 CTGAATATGTTTCCATCACACAATTTGTTACTTCTCAGTGAATTTCTTCAAAACCATTTGCA 60

```


Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 457.
 Location/Qualifiers
 1. 510
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2772915"
 /clone_lib="NCI CGAP Kid11"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo." .
 BASE COUNT 137 a 85 c 115 g 173 t
 ORIGIN
 Query Match 17.4%; Score 497; DB 10; Length 510;
 Best Local Similarity 99.0%; Pred. No. 1.1e-80;
 Matches 500; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2319 CTTTCTCGAGTGATCTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTT 2378
 DB 510 CTTTCTCGAGTGATCTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTT 451
 QY 2379 AGAGATTGATACAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACACATTC 2438
 DB 450 AGAGATTGATACAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACACATTC 391
 QY 2439 ATGAAGATGCCATGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCGGTGTCAGCA 2498
 DB 390 ATGAAGATGCCATGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCGGTGTCAGCA 331
 QY 2499 GGAAAAAGATCAAGCCTGCCACGATGGCTGCTGCTCTTGTAGCCCAACCATGAGAAG 2558
 DB 330 GGAAAAAGATCAAGCCTGCCACGATGGCTGCTGCTCTTGTAGCCCAACCATGAGAAG 271
 QY 2559 CAAGACGCTTAAAGCTTCTATCCCAATATACAGGGAAAAACGTTGATGATCT 2618
 DB 270 CAAGACGCTTAAAGCTTCTATCCCAATATACAGGGAAAAACGTTGATGATCT 211
 QY 2619 GAAGCTTACTATGACGCTTACAAACAGCCTTAGTAATTAACCACTTTTATACCAATAAA 2678
 DB 210 GAAGCTTACTATGACGCTTACAAACAGCCTTAGTAATTAACCACTTTTATACCAATAAA 151
 QY 2679 TTTTCAATATTTACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2738
 DB 150 TTTTCAATATTTGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 91
 QY 2739 TCAAGCTGTTTTATACATAGAAATCAATACAGCTTTAATTAATTAATTAATTAATTAATTA 2798
 DB 90 TCAAGCTGTTTTATACATAGAAATCAATACAGCTTTAATTAATTAATTAATTAATTAATTA 31
 QY 2799 GATAATGCAACATAAAGCATCTTC 2823
 DB 30 GATAATGCAACATAAAGCATCTTC 6

RESULT 11
 LOCUS BF110326/c
 DEFINITION 736f01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566736 3', mRNA sequence.
 ACCESSION BF110326
 VERSION BF110326.1 GI:10940016
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 509)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 470.
 Location/Qualifiers
 1. 509
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 /db_xref="taxon:9606"
 /clone="IMAGE:3566736"
 /clone_lib="NCI_CGAP_Lu24"
 /tissue_type="carcinoid"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo." .
 BASE COUNT 132 a 84 c 113 g 180 t
 ORIGIN
 Query Match 17.3%; Score 493; DB 12; Length 509;
 Best Local Similarity 98.0%; Pred. No. 6.1e-80;
 Matches 499; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 2326 GCAGTGATCTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTTAGAGAGA 2385
 DB 509 GCAGTGATCTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTTAGAGAGA 450
 QY 2386 TTGTACAAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACCACTTCATGAAGG 2445
 DB 449 TTGTACAAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACCACTTCATGAAGG 390
 QY 2446 ATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGTCAGCAGGAAAA 2505
 DB 389 ATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGTCAGCAGGAAAA 330
 QY 2506 GATCAAGCTGTCACGATGGCTGCTCTCTTGTAGCCCAACCCATGAGAAGCAGAGAGA 2565
 DB 329 GATCAAGCTGTCACGATGGCTGCTCTCTTGTAGCCCAACCCATGAGAAGCAGAGAGA 270
 QY 2566 CCTTAAAGGCTTCTATCCCAACCAATTACAGGGAAAAACGTTGATGATGATGATGATGATGAT 2625
 DB 269 CCTTAAAGGCTTCTATCCCAACCAATTACAGGGAAAAACGTTGATGATGATGATGATGATGAT 210

Qy	2626	ACTATGCAGCCTCAAAACAGCCTTAGTAATTAATAAACATTTTATACCAATAAAATTTTCAA	2685
Db	209	ACTATGCAGCCTCAAAACAGCCTTAGTAATTAATAAACATTTTATACCAATAAAATTTTCAA	150
Qy	2686	ATATTACTTAACCTATGTAGCAATTAACCTAAGCTTGGAACTTACATTTTACAACTTTCAAGC	2745
Db	149	ATATTGCTTAACCTATGTAGCAATTAACCTAAGCTTGGAACTTACATTTTACAACTTTCAAGC	90
Qy	2746	TGTTTTATACATAGAAATCAATTACAGCTTTAAATTGAAACTGTAAACCATTTTGATAATG	2805
Db	89	TGTTTTATACATAGAAATCAATTACAGCTTTAAATTGAAACTGTAAACCATTTTGATAATG	30
Qy	2806	CAACAATAAAGCATCTTCCAAAAA 2834	
Db	29	CAACAATAAAGCATCTTTCAGCCAAACAAA 1	
RESULT 12			
LOCUS	BE466508/c		
DEFINITION	BE466508	502 bp	mRNA linear EST 27-JUL-2000
ACCESSION	hx93n01.x1	NCI_CGAP_Kid11	Homo sapiens cDNA clone IMAGE:3195409 3',
KEYWORDS	BE466508		mRNA sequence.
SOURCE	BE466508.1	GI:9512206	
ORGANISM	EST.		
	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 502)		
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: Gqaps-x@mail.nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.		
	Emmert-Buck, M.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL, send email to:		
	infoimage.llnl.gov		
	Seq primer: -40UP from Gibco		
	High quality sequence stop: 466.		
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source	1. 502		
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	/clone="IMAGE:3195409"		
	/clone_lib="NCI_CGAP_Kid11"		
	/lab_host="DH10B"		
	/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with		
	a modified polylinker; Site 1: Not 1; Site 2: Eco RI;		
	Plasmid DNA from the normalized library NCI_CGAP_Kid3 was		
	prepared, and ss circles were made in vitro. Following HAP		
	purification, this DNA was used as tracer in a subtractive		
	hybridization reaction. The driver was PCR-amplified cDNAs		
	from a pool of 5,000 clones made from the same library		
	(cloneIDs 1322376-1323911, 1456007-1456775, and		
	1500552-1502855). Subtraction by Bento Soares and M.		
	Patricia Bonaldo."		
BASE COUNT	130 a	87 c	114 g 171 t
ORIGIN			
Query Match	16.7%	Score 477.4;	DB 10; Length 502;
Best Local Similarity	97.8%	Pred No. 4.3e-77;	
Matches 484; Conservative	0;	Mismatches 11;	Indels 0; Gaps 0;
Qy	2327	CAGTGATCTAAGAGCGAGATTCATCTGCACAAATACGTGCTGCTTACTTTAGAGAGAT	2386

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 151 a 136 c 166 g 162 t
ORIGIN
Query Match 16.7%; Score 476.8; DB 10; Length 615;
Best Local Similarity 84.8%; Pred. No. 5.1e-77;
Matches 599; Conservative 0; Mismatches 12; Indels 95; Gaps 2;
Qy 1491 TGTACCTGTAGATAGTACCTAGCCCTTTAGGTAAGCGAACTGTATGTAGTAACCT 1550
Db 1 TCTACCTGTGAATATAGTACCTAGCCCTTTAGGTAAGCGAACTGTATGTAGTAACCT 60
Qy 1551 GTACAAAGTTTAGTTTCAGACCCCGGAGTCTTGGGCATGTGGTCTCGGTCACCTGGTT 1610
Db 61 GTACAAAGTTTAGTTTCAGACCCCGGAGTCTTGGGCATGTGGTCTCGGTCACCTGGTT 120
Qy 1611 TTGACCTTTAGGCTTTTGTACAGATGTGTGACCAAGGGAATATGTCATGCAACACTA 1670
Db 121 TTGACCTTTAGGCTTTTGTACAGATGTGTGACCAAGGGAATATGTCATGCAACACTA 180
Qy 1671 GAGGTAGGGCGGAGCCAGAAAGGGAAGTTTGGCTGAAGTGGAGTCTTGTGTGAGA 1730
Db 181 GAGGTAGGGCGGAGGAGCAAGAAAGGGAAGTTTGGCTGAAGTGGAGTCTTGTGTGAGA 233
Qy 1731 TTTTGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1790
Db 234 ----- 233
Qy 1791 TATTTTCTTACTTGTGGGAGGAGTGCATCCGACATPAAAGGAACAGTTGTCTTGCCCA 1850
Db 234 -----GCGACTGCATCCGACATPAAAGGAACAGTTGTCTTGCCCA 274
Qy 1851 CAACAGGCGTCCCTTTCCTCTGATATACAAAGCAAGCCGGAGGCTGGTGGCT 1910
Db 275 CAACAGGCGTCCCTTTCCTCTGATATACAAAGCAAGCCGGAGGCTGGTGGCT 334
Qy 1911 CTCCT 1970
Db 335 CTCCT 394
Qy 1971 TGGAGGACGAAAGATCAAGAAAGTCTCTCTTTTACCAACACACTACTGCCCCCAAT 2030
Db 395 TGGAGGACGAAAGATCAAGAAAGTCTCTCTTTTACCAACACACTACTGCCCCCAAT 454
Qy 2031 AAGGTTCTTGTGTTTACCCTCTGAATATGTTTCCATCACACATTTGTTACTTCACT 2090
Db 455 AAGGTTCTTGTGTTTACCCTCTGAATATGTTTCCATCACACATTTGTTACTTCACT 514
Qy 2091 GAATTTCTTCAAAACCATTTGCAGAGTGAAGTCACTCTTGAAGTGGCAGAAAAAGAAA 2150
Db 515 GAATTTCTTCAAAACCATTTGCAGAGTGAAGTCACTCTTGAAGTGGCAGAAAAAGAAA 565
Qy 2151 ATAGCAGAGATGGTCCAGTGCAGTGGTGGCCACTCAAAAGAG 2196
Db 566 GTAGCAGAGATGGTCCAGTGCAGTGGTGGCCACTCGTGCATGG 611

RESULT 14
BF064177/c
LOCUS 7h95b11.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3323709 3',
DEFINITION mRNA sequence.
ACCESSION BF064177
VERSION BF064177.1 GI:10823087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ilian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 400.

FEATURES
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purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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VERSION AA514396.1 GI:2253996
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SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40ml3 fwd. ET from Amersham
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was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization."
BASE COUNT 130 a 81 c 109 g 168 t
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Matches 478; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Job time : 3998.87 secs

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
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RESULT 3

RESULT 3
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; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby

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; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
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;	APPLICANT:	Gurney, Austin	
;	APPLICANT:	Li, Hanzhong	
;	APPLICANT:	Hillan, Kenneth J.	
;	APPLICANT:	Hymowitz, Sarah	
;	APPLICANT:	Tumaas, Daniel	
;	APPLICANT:	Starovaanik, Melissa.	
;	APPLICANT:	Vanlookeren, Menno	
;	APPLICANT:	Vandlen, Richard	
;	APPLICANT:	Watanabe, Colin	
;	APPLICANT:	Williams, P.Mickey	
;	APPLICANT:	Wood, William	
;	APPLICANT:	Yansura, Daniel	
;	TITLE OF INVENTION:	IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF	
;	FILE REFERENCE:	P1381R1C1P4(US)	
;	CURRENT APPLICATION NUMBER:	US/10/000,157	
;	CURRENT FILING DATE:	2001-10-30	
;	PRIOR APPLICATION NUMBER:	60/085579	
;	PRIOR FILING DATE:	1998-05-15	
;	PRIOR APPLICATION NUMBER:	60/113621	
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;	PRIOR APPLICATION NUMBER:	60/130232	
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;	PRIOR FILING DATE:	2001-08-13	
;	PRIOR APPLICATION NUMBER:	09/931836	
;	PRIOR FILING DATE:	2001-08-16	
;	PRIOR APPLICATION NUMBER:	PCT/US99/05028	
;	PRIOR FILING DATE:	1999-03-08	
;	PRIOR APPLICATION NUMBER:	PCT/US99/10733	
;	PRIOR FILING DATE:	1999-05-14	
;	PRIOR APPLICATION NUMBER:	PCT/US99/31274	


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, PRIOR APPLICATION NUMBER: PCT/US00/15264
, PRIOR FILING DATE: 2000-06-02
, PRIOR APPLICATION NUMBER: US 60/213,087
, PRIOR FILING DATE: 2000-06-22
, PRIOR APPLICATION NUMBER: US 09/644,848
, PRIOR FILING DATE: 2000-08-22
, PRIOR APPLICATION NUMBER: PCT/US00/23328
, PRIOR FILING DATE: 2000-08-24
, PRIOR APPLICATION NUMBER: US 60/242,837
, PRIOR FILING DATE: 2000-10-24
, PRIOR APPLICATION NUMBER: PCT/US00/30873
, PRIOR FILING DATE: 2000-11-10
, PRIOR APPLICATION NUMBER: US 60/253,646
, PRIOR FILING DATE: 2000-11-28
, PRIOR APPLICATION NUMBER: PCT/US00/32678
, PRIOR FILING DATE: 2000-12-01
, NUMBER OF SEQ ID NOS: 39
, SEQ ID NO 11
, LENGTH: 1515
, TYPE: DNA
, ORGANISM: Homo Sapien
US-09-747-259-11

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Query Match	26.7%	Score 763.4	DB 9	Length 1515
Best Local Similarity	99.9%	Pred. No. 3.3e-194		
Matches 764	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 1779	CAGCTGACTCCATATTTTCTACTTTGTGGCAGCGACTCATCCGACATATAAGGAACAGTT	1838		
Db 751	CAGCTGACTCCATATTTTCTACTTTGTGGCAGCGACTCATCCGACATATAAGGAACAGTT	810		
Qy 1839	GTGCTCTGCCCAACAAACAGGCGTCCCTTTCCCTCTGGTAACAAACAAAGCAAGCGCGGA	1898		
Db 811	GTGCTCTGCCCAACAAACAGGCGTCCCTTTCCCTCTGGTAACAAACAAAGCAAGCGCGGA	870		
Qy 1899	GGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCACATGGTGTGGTGGCAGGG	1958		
Db 871	GGCTGGCTGCCTCTCCTCTGCTGTCTGCTGGTGGCCACATGGTGTGGTGGCAGGG	930		
Qy 1959	ATCTATCTAAATGTGGAGGCACGAAGGATCAAGAGACTTCCTTTCTACACACACACTA	2018		
Db 931	ATCTATCTAAATGTGGAGGCACGAAGGATCAAGAGACTTCCTTTCTACACACACACTA	990		
Qy 2019	CTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACAATTT	2078		
Db 991	CTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACAATTT	1050		
Qy 2079	TGTTTACTTCAGTGAATTTCTTCAAACCATTTGCAGAAGTGAGGTCATCCTTGAAGAAGTG	2138		
Db 1051	TGTTTACTTCAGTGAATTTCTTCAAACCATTTGCAGAAGTGAGGTCATCCTTGAAGAAGTG	1110		
Qy 2139	CAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCACATCAAAAGAAGCA	2198		
Db 1111	CAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCACATCAAAAGAAGCA	1170		
Qy 2199	GCAGACAAGTCGTCTTCCCTTTTCCAAATGACGTCAACAGTGTGTGGATGGTACCTGT	2258		
Db 1171	GCAGACAAGTCGTCTTCCCTTTTCCAAATGACGTCAACAGTGTGTGGATGGTACCTGT	1230		
Qy 2259	GGCAAGCAGGAGGCGAGTCCAGTGAGAACTCTCAAGACCTCTTCCCTTGCCTTTTAAAC	2318		
Db 1231	GGCAAGCAGGAGGCGAGTCCAGTGAGAACTCTCAAGACCTCTTCCCTTGCCTTTTAAAC	1290		
Qy 2319	CTTTTCTGCAGTGATCTAAGAAGCCAGATTCAATCTGCACAAATACGTGGTGTCTACTTT	2378		
Db 1291	CTTTTCTGCAGTGATCTAAGAAGCCAGATTCAATCTGCACAAATACGTGGTGTCTACTTT	1350		
Qy 2379	AGAGAGATTGATCAAAAGACGATTTACAACTGCTCTCAGTGTCTGCCCAAGTACCACTTC	2438		
Db 1351	AGAGAGATTGATCAAAAGACGATTTACAACTGCTCTCAGTGTCTGCCCAAGTACCACTTC	1410		
Qy 2439	ATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTTCCAATGTCAAGCAGCAGGTGTCAACA	2498		

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Db 1411 ATGAGAGTCCACTGCTTCTGTGTGCAGNACTTCTCCATGTCACAGCAGGTGTCAGCA 1417
Qy 2499 GGAAAAGATCACAAAGCCTGCCACGATGGCTGCTCTCTCTTTGTAG 2543
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Db 1471 GGAAAAGATCACAAAGCCTGCCACGATGGCTGCTCTCTCTTTGTAG 1515
   |||||

RESULT 11
US-10-174-590-399
; Sequence 399, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Destoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-399

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Query Match	26.7%	Score 763.4	DB 9	Length 1515
Best Local Similarity	99.9%	Pred. No. 3.3e-194		
Matches 764	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	1779	CAGCTGACTCCATATTTTCCTACCTGTGTGGCAGCAGCTGCATCCGACACATAAAGGAACAGTT	1838	
Db	751			
Qy	1839	GTGCTCTGCCACAAAACAGGGCGTCCCTTTCCTCTGGATAACAACAAAAGCAAGCCGGGA	1898	
Db	811			
Qy	1899	GGCTGGTGCCCTCTCCTCTCTCTCTGTGTGGCCACATGGGTGCTGGTGGCAGGG	1958	
Db	871	GGCTGGTGCCCTCTCCTCTCTCTCTGTGTGGCCACATGGGTGCTGGTGGCAGGG	930	
Qy	1959	ATCTATCTAATGTGGAGGCACGAAGGATCAAGAAGACTTCCCTTTCTACACACACACTA	2018	
Db	931	ATCTATCTAATGTGGAGGCACGAAGGATCAAGAAGACTTCCCTTTCTACACACACACTA	990	
Qy	2019	CTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATT	2078	
Db	991	CTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATT	1050	
Qy	2079	TGTTACTTCACTGAATTTCTTCAAAACCATTTGCAGAAGTGAGGTCACTCTTTGAAAAGTGG	2138	
Db	1051	TGTTACTTCACTGAATTTCTTCAAAACCATTTGCAGAAGTGAGGTCACTCTTTGAAAAGTGG	1110	
Qy	2139	CAGAAAAGAAAATAGCAGAGATGGGTCCAGTCAGTGGCTTGGCACTCAAAAAGAGGCA	2198	
Db	1111	CAGAAAAGAAAATAGCAGAGATGGGTCCAGTCAGTGGCTTGGCACTCAAAAAGAGGCA	1170	
Qy	2199	GCAGACAAGTCGTCTTCTTCTTCCAAATGACCTCAACAGTGTGCGATGGTACCTGT	2258	
Db	1171	GCAGACAAGTCGTCTTCTTCTTCCAAATGACCTCAACAGTGTGCGATGGTACCTGT	1230	
Qy	2259	GGCAAGACGAGGCGAGTCGCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAAAC	2318	

Db 1231 GGCAGAGCGAGGCGAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGGCTTTAAC 1290
QY 2319 CTTTCTGCGAGTGATCTAAGAACCCAGATTCACTGTCACAAATACGTGGTGGTCTACTTT 2378
Db 1291 CTTTCTGCGAGTGATCTAAGAACCCAGATTCACTGTCACAAATACGTGGTGGTCTACTTT 1350
QY 2379 AGAGAGATTGATCAAAAGACGATTACATGCTCTAGTGTCTGCCCCAAGTACCACTTC 2438
Db 1351 AGAGAGATTGATCAAAAGACGATTACATGCTCTAGTGTCTGCCCCAAGTACCACTTC 1410
QY 2439 ATGAAGATTGATCAAAAGACGATTACATGCTCTAGTGTCTGCCCCAAGTACCACTTC 2498
Db 1411 ATGAAGATTGATCAAAAGACGATTACATGCTCTAGTGTCTGCCCCAAGTACCACTTC 1470
QY 2499 GGAAAAGATCAAAAGACGATTACATGCTCTAGTGTCTGCCCCAAGTACCACTTC 2543
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RESULT 12

US-10-176-758-399
; Sequence 399, Application US/10176758
; Publication No. US2003008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; PRIOR FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-399

Query Match 26.7%; Score 763.4; DB 9; Length 1515;
Best Local Similarity 99.9%; Pred. No. 3.3e-194;
Matches 764; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1779 CAGCTGACTCCATATTTTCTACTTGTGGCAGGACTGTCATCGACATAAAGAACAGTT 1838
Db 751 CAGCTGACTCCATATTTTCTACTTGTGGCAGGACTGTCATCGACATAAAGAACAGTT 810
QY 1839 GTGCTCTGCCCAAAACAGCGTCCCTTTCCCTCTGGATAAACAAGAACGCGGGA 1898
Db 811 GTGCTCTGCCCAAAACAGCGTCCCTTTCCCTCTGGATAAACAAGAACGCGGGA 870
QY 1899 GGCTGGCTGCCTCTCTCTGCTGTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGG 1958
Db 871 GGCTGGCTGCCTCTCTCTGCTGTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGG 930
QY 1959 ATCTATCTAATGTGGAGGACAAAGGATCAAGAACACTCTTTTCTACCACTCACTA 2018
Db 931 ATCTATCTAATGTGGAGGACAAAGGATCAAGAACACTCTTTTCTACCACTCACTA 990
QY 2019 CTGCCCCCATTAAGTCTCTGTGGTTTACCATCTGGAATATGTTTCCATCACAAATT 2078
Db 991 CTGCCCCCATTAAGTCTCTGTGGTTTACCATCTGGAATATGTTTCCATCACAAATT 1050

QY 2079 TGTACTTCACTGAATTTCTTCAAAACCAATTCGAGAGTGAAGTATCTTGTGAAAAGTGG 2138
Db 1051 TGTACTTCACTGAATTTCTTCAAAACCAATTCGAGAGTGAAGTATCTTGTGAAAAGTGG 1110
QY 2139 CAGAAAAGAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCCTCAAAAGAACAGGCA 2198
Db 1111 CAGAAAAGAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCCTCAAAAGAACAGGCA 1170
QY 2199 GCAGACAAAGTCTCTTCTTCTTCAATGACGTCAACAGTGTGTGCGATGGTACCTGT 2258
Db 1171 GCAGACAAAGTCTCTTCTTCTTCAATGACGTCAACAGTGTGTGCGATGGTACCTGT 1230
QY 2259 GCGAAGAGCGAGGCGAGTCCAGTGCAGTGAAGTCTCAAGACTCTTCCCCCTTGGCTTTAAC 2318
Db 1231 GCGAAGAGCGAGGCGAGTCCAGTGCAGTGAAGTCTCAAGACTCTTCCCCCTTGGCTTTAAC 1290
QY 2319 CTTTCTGCGAGTGATCTAAGAACCCAGATTCACTGTCACAAATACGTGGTGGTCTACTTT 2378
Db 1291 CTTTCTGCGAGTGATCTAAGAACCCAGATTCACTGTCACAAATACGTGGTGGTCTACTTT 1350
QY 2379 AGAGAGATTGATCAAAAGACGATTCAATGCTCTCAAGTGTGTGCCCCAAGTACCACTTC 2438
Db 1351 AGAGAGATTGATCAAAAGACGATTCAATGCTCTCAAGTGTGTGCCCCAAGTACCACTTC 1410
QY 2439 ATGAAGATTGATCAAAAGACGATTCAATGCTCTCAAGTGTGTGCCCCAAGTACCACTTC 2498
Db 1411 ATGAAGATTGATCAAAAGACGATTCAATGCTCTCAAGTGTGTGCCCCAAGTACCACTTC 1470
QY 2499 GGAAAAGATCAAAAGACGATTCAATGCTCTCAAGTGTGTGCCCCAAGTACCACTTC 2543
Db 1471 GGAAAAGATCAAAAGACGATTCAATGCTCTCAAGTGTGTGCCCCAAGTACCACTTC 1515

RESULT 13

US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157

Query Match 26.7%; Score 763.4; DB 9; Length 1515;
Best Local Similarity 99.9%; Pred. No. 3.3e-194;
Matches 764; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1779 CAGCTGACTCCATATTTTCTACTTGTGGCAGGACTGTCATCGACATAAAGAACAGTT 1838
Db 751 CAGCTGACTCCATATTTTCTACTTGTGGCAGGACTGTCATCGACATAAAGAACAGTT 810
QY 1839 GTGCTCTGCCCAAAACAGCGTCCCTTTCCCTCTGGATAAACAAGAACGCGGGA 1898
Db 811 GTGCTCTGCCCAAAACAGCGTCCCTTTCCCTCTGGATAAACAAGAACGCGGGA 870
QY 1899 GGCTGGCTGCCTCTCTCTGCTGTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGG 1958

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	53	1.9	6243	2	US-09-056-075-1
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3	49.8	1.7	1776	3	US-08-655-352-10
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5	49.8	1.7	1776	4	US-09-257-825B-10
6	49.4	1.7	240	1	US-08-628-417-6
7	49.2	1.7	1100	4	US-07-861-458C-4
8	49	1.7	2836	3	US-08-747-221B-24
9	49	1.7	2836	3	US-08-747-221B-26
10	49	1.7	2836	4	US-09-005-051-24
11	49	1.7	2836	4	US-09-005-051-26
12	49	1.7	5173	1	US-08-242-677-1
13	48.4	1.7	2447	2	US-09-014-969-14
14	48.2	1.7	991	3	US-08-924-747-25
15	48.2	1.7	991	4	US-09-247-373B-25
16	48.2	1.7	991	4	US-09-296-715-25
17	47.6	1.7	2671	6	5168051-9
18	47.4	1.7	974	2	US-08-504-459-13
19	47.4	1.7	1578	4	US-09-416-050A-1
20	47.4	1.7	1578	4	US-09-664-800-1
21	47.4	1.7	1578	4	US-09-665-309-1
22	47.4	1.7	1578	4	US-09-661-569-1
23	47.4	1.7	1720	4	US-09-227-357-139
24	47.4	1.7	19557	5	PCT-US92-06300-1
25	47.2	1.7	593	4	US-09-385-982-262
26	47.2	1.7	658	4	US-08-998-416-595
27	47	1.6	1582	3	US-08-545-196B-10

28	47	1.6	1582	3	US-08-545-196B-12	Sequence 12, Appl
29	47	1.6	2095	4	US-09-227-357-31	Sequence 31, Appl
30	47	1.6	2202	4	US-09-465-558-59	Sequence 59, Appl
c 31	46.4	1.6	602	1	US-08-764-100-8	Sequence 8, Appl
32	46.4	1.6	642	1	US-08-764-100-13	Sequence 13, Appl
c 33	46.4	1.6	643	1	US-08-764-100-7	Sequence 7, Appl
34	46.4	1.6	2378	4	US-08-802-805D-20	Sequence 20, Appl
c 35	46.4	1.6	2993	1	US-08-764-100-2	Sequence 2, Appl
36	46.4	1.6	2993	1	US-08-764-100-10	Sequence 10, Appl
c 37	46.4	1.6	3000	1	US-08-764-100-9	Sequence 9, Appl
38	46.4	1.6	3001	1	US-08-764-100-1	Sequence 1, Appl
c 39	46.2	1.6	7859	2	US-07-854-596B-4	Sequence 4, Appl
40	46.2	1.6	7859	2	US-08-450-905B-15	Sequence 15, Appl
41	46.2	1.6	7859	3	US-07-982-759F-15	Sequence 15, Appl
42	46	1.6	1512	2	US-08-909-965C-8	Sequence 8, Appl
43	46	1.6	2435	4	US-09-306-593-1	Sequence 1, Appl
44	45.8	1.6	796	1	US-08-104-073-2	Sequence 2, Appl
45	45.8	1.6	1700	2	US-08-897-340-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-056-075-1
; Sequence 1, Application US/09056075
; Patent No. 5955368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marite
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium
; TITLE OF INVENTION: Species
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
; OTHER INFORMATION: plasmid RP4"
US-09-056-075-1

Query Match 1.9%; Score 53; DB 2; Length 6243;
Best Local Similarity 49.5%; Pred. No. 0.00027;

Matches 137; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 2580 TATCCACCACCAATTTACAGGGAAGAAACGTGTGATGATCCTGAAGCTTACTATGACAGCTAC 2639
 DB 1118 TATCTTTTACAACCTCCCAAAAGAAAGAGACAGGTACAAAGTACCCCTATATACAGCGTA 1177
 QY 2640 AAACAGCCTTAGTAATTTAAACCAATTTTATACCAATATAAATTTTCAAAATATTACTAACTAA 2699
 DB 1178 AAAAAATAGGGTAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAAT 1237
 QY 2700 TGTAGCAATTAACGATTTGGAACCTACATTTTACAACTTTCAAGCTGTTTATACATAG 2759
 DB 1238 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1297
 QY 2760 AATCAATTACAGCTTTAATTTGAACCTGTAACCAATTTTGTATATGCAACAATAAGCAT 2819
 DB 1298 AATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1357
 QY 2820 CTTCACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2856
 DB 1358 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1394

RESULT 2
 US-08-487-826B-13
 ; Sequence 13, Application US/08487826B
 ; Patent No. 5993827
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Kim L.
 ; APPLICANT: Chitnis, Chetan
 ; APPLICANT: Miller, Louis H.
 ; APPLICANT: Peterson, David S.
 ; APPLICANT: Su, Xin-zhaun
 ; APPLICANT: Wellens, Thomas E.
 ; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 ; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe Martens Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,826B
 ; FILING DATE: 10-SEP-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israel, Ned
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: NIH121.001CPI
 ; TELEPHONE: (619) 235-8550
 ; TELEFAX: (619) 235-0176
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19124 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-487-826B-13

Query Match 1.8%; Score 50; DB 2; Length 19124;
 Best Local Similarity 51.8%; Pred. No.. 0.0033;

Matches 113; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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 QY 2698 AATGTAGCAATTAACGATTTGGAACCTACATTTTACAACTTTCAAGCTGTTTATACAT 2757
 DB 15515 GGAGAAAAATTTTATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15574
 QY 2758 AGAAATCAATTAACGCTTTAATTTGAAAACTGTAACCAATTTTGTATATGCAACAATAAGC 2817
 DB 15575 AAAAAATGAAAAAGATTATCAAAAAAATTTAAAAAATAAATTTTATATATAAAAAAATAATGA 15634
 QY 2818 ATCTTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2855
 DB 15635 TTATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15672

RESULT 3
 US-08-655-352-10
 ; Sequence 10, Application US/08655352
 ; Patent No. 6077991
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
 ; APPLICANT: Shameekumar Patil, Daisuke Takezawa
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ; ADDRESSEE: Winston, LLP
 ; STREET: One World Trade Center
 ; STREET: 121 S.W. Salmon Street
 ; CITY: Portland
 ; STATE: Oregon
 ; COUNTRY: United States of America
 ; ZIP: 97204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3-1/2 inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/655,352
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/323,449
 ; FILING DATE: October 14, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dow, Alan. E.
 ; REGISTRATION NUMBER: 35,123
 ; REFERENCE/DOCKET NUMBER: 4630-45000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1776 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double stranded
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; DESCRIPTION: Tobacco CcAmk cDNA and deduced amino-acid
 ; DESCRIPTION: sequence
 ; FEATURE:
 ; NAME/KEY: protein-coding sequence (not including
 ; NAME/KEY: stop codon)
 ; LOCATION: nucleotides 20-1570
 ; US-08-655-352-10

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Db 1728 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1776

RESULT 5
US-09-257-825B-10
; Sequence 10, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiyah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-257-825B-10

Query Match 1.7%; Score 49.8; DB 4; Length 1776
Best Local Similarity 66.1%; Pred. No. 0.001;
Matches 72; Conservative 0; Mismatches 37; Indels

QY 2748 TTTTATACATAGAAATCAATTACAGCTTTAATTCGAAAACTGTAAACCATTTTGTATGTTT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1668 TTTTATCACTACTCGTAAAGATCCCTTTAATTAATTCGGAAGCCTTTATGTGTTT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2808 ACAATAAAGCATCTTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1728 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1776

RESULT 6
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESSEE: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELEPHONE: 410-671-1158

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; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match 1.7%; Score 49.4; DB 1; Length 240;
Best Local Similarity 51.6%; Pred. No. 0.00046;
Matches 113; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 2638 ACAACAGCCTTAGTAATTAACATTTTATACCAATTAATTTTCAATATTTACTAACT 2697
Db 6 ATAAAGACATAAACTTTAGAAATATTTTACTAAAAAATAAAAAAAAAAAAAAAAAA 65

QY 2698 AATGTAGCATTAACACGATTGGAACATACATTTCAACTTCAAGCTGTTTATACAT 2757
Db 66 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 125

QY 2758 AGAAATCAATACAGCTTTAATTTGAAACCTGTACCATTTTGATAATGCAACAATAAGC 2817
Db 126 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 185

QY 2818 ATCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
Db 186 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 224

RESULT 7
US-07-861-458C-4
; Sequence 4, Application US/07861458C
; Patent No. 6232061
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark Andrew
; APPLICANT: Johnson, Carl D.
; TITLE OF INVENTION: HOMOLOGY CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861.458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-861-458C-4

Query Match 1.7%; Score 49.2; DB 4; Length 1100;
Best Local Similarity 73.3%; Pred. No. 0.0012;
Matches 63; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2771 AGCTTTAATGAAACTGTAAACCACTTTTGATAATGCAACAATAAAGCATCTTCCAAAAA 2830
Db 997 ATCTCTAATTTGTATAGTAGCTTTTGTATTAATAAAAAAAAAAAAAAAAAA 1056

QY 2831 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
Db 1057 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1082

RESULT 8
US-08-747-221B-24
; Sequence 24, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2836 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..1889
US-08-747-221B-24

Query Match 1.7%; Score 49; DB 3; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0022;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 2712 TAACGATTGGAACACTACATTTTACAACTTCAAGCTGTTTTATACATAGAAATCAATTACA 2771
Db 2688 TATGGAATTATGTCAACATGTAAATACAAATCGGTGTTTAAATAATCTGTATTAAA 2747

QY 2772 GCTTTAATGAAACTGTAAACCTTTTGTATTAATGCAACAATAAAGCATCTTCCAAAAA 2831
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Db 2748 ATTGTTATATAAATCTGAATAATGCTACTTTTAAAGTAAATAAAAAAAAAAAAAAAAAAAAAA 2807
QY 2832 AAAAAAAAAAAAAAAAAAAAAA 2856
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Db 2808 AAAAAAAAAAAAAAAAAAAAAA 2832

RESULT 9
US-08-747-221B-26/c
; Sequence 26, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2836 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-747-221B-26

Query Match 1.7%; Score 49; DB 3; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0022;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 2712 TAACGATTGGAACACTACATTTCACAACTTCAAGCTGTTTATACATAGAAATCAATTACA 2771
|||
Db 149 TATGATTAAATGTCACATGTAATAATACAAATGCGGTGTTTAAATAATAATCTGTATTAAA 90
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QY 2772 GCTTTAATTGAAACCTGTAACCATTTTGATATGCAACAATAAAGCATCTTCCAAAAA 2831
|||
Db 89 ATTGTTATATAAATCTGTAATAATGCTACTTTTAAAGTAAATAAAAAAAAAAAAAAAAAAAAAA 30
|||

QY 2832 AAAAAAAAAAAAAAAAAAAAAA 2856
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 10
US-09-005-051-24
; Sequence 24, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2836 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..1889
US-09-005-051-24

Query Match 1.7%; Score 49; DB 4; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0022;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 2712 TAACGATTGGAACACTACATTTCACAACTTCAAGCTGTTTATACATAGAAATCAATTACA 2771
|||
Db 2688 TATGATTAAATGTCACATGTAATAATACAAATGCGGTGTTTAAATAATAATCTGTATTAAA 2747
|||

QY 2772 GCTTTAATTGAAACCTGTAACCATTTTGATATGCAACAATAAAGCATCTTCCAAAAA 2831
|||
Db 2748 ATTGTTATATAAATCTGTAATAATGCTACTTTTAAAGTAAATAAAAAAAAAAAAAAAAAAAAAA 2807
|||

QY 2832 AAAAAAAAAAAAAAAAAAAAAA 2856
|||||
Db 2808 AAAAAAAAAAAAAAAAAAAAAA 2832

RESULT 11
US-09-005-051-26/c
; Sequence 26, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,677
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4863
; US-08-242-677-1

Query Match 1.7%; Score 49; DB 1; Length 5173;
Best Local Similarity 69.1%; Pred. No. 0.0031;
Matches 67; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2760 AAATCAATTACAGCTTTAATTGAAACCTGTAACCATTTTGATATGCAACAATAAAGCAT 2819
Db 5059 AATGTGATTTCTTCCTTTAATAAAATATTTTAAGCAATTTGTCCAATAAAAAAAAAAAAAA 5118

Qy 2820 CTTCCAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
Db 5119 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5155

RESULT 13
US-09-014-969-14
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284

```

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; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match      1.7%; Score 48.4; DB 2; Length 2447;
Best Local Similarity 50.4%; Pred. No. 0.003;
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 2623 CTTACTATGAGCCTCAACAGCCTTAGTAATTAACCAATTTTACCAATAAAATTTT 2682
Db 2214 CTTAAATGTGACAAATAAACCTTTTGGGAGAAAAAATAAATAAATAAATAAATAA 2273

QY 2683 CAAATATTACTACTAGTACGATTAACTTAACGATTGGAACTACATTACCACTTCAA 2742
Db 2274 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2333

QY 2743 AGCTGTTTATACATGAATCAATACAGCTTTAATTCGAAACTGTAACCATTTTGATA 2802
Db 2334 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2393

QY 2803 ATGCAACAATAAGCATCTTCCAAAAAATAAATAAATAAATAAATAAATAAATAA 2856
Db 2394 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2447

RESULT 14
US-08-924-747-25
; Sequence 25, Application US/08924747
; Patent No. 6063570
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: E.I. DU PONT DE NEMOURS AND COMPANY
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,747
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; ORIGINAL SOURCE:
; TISSUE TYPE: SOYBEAN
; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
US-08-924-747-25

Query Match      1.7%; Score 48.2; DB 3; Length 991;
Best Local Similarity 69.9%; Pred. No. 0.0021;
Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2764 CAATTACAGCTTTAATTTGAAACTGTAAACCATTTTGATAATGCAACAATAAAGCATCTTC 2823
Db 891 CTATTTTAAATTTTAACTAAATAAAGTGTCAGTTTAAAAAATAAATAAATAAATAA 950

QY 2824 CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2856
Db 951 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 983

RESULT 15
US-09-247-373B-25
; Sequence 25, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; CURRENT FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; TYPE: DNA
; ORGANISM: SOYBEAN
US-09-247-373B-25

Query Match      1.7%; Score 48.2; DB 4; Length 991;
Best Local Similarity 69.9%; Pred. No. 0.0021;
Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2764 CAATTACAGCTTTAATTTGAAACTGTAAACCATTTTGATAATGCAACAATAAAGCATCTTC 2823
Db 891 CTATTTTAAATTTTAACTAAATAAAGTGTCAGTTTAAAAAATAAATAAATAAATAA 950

QY 2824 CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2856
Db 951 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 983

Search completed: May 28, 2003, 10:21:46
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GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:36:08 ; Search time 577.385 Seconds
(without alignments)
11139.370 Million cell updates/sec

Title: US-09-778-971-2

Perfect score: 2856

Sequence: 1 cggcgatcgtcgtcgtcgtg.....aaaaaaaaaaaaaaaaaaaaa 2856

Scoring table:

IDENTITY_NUC

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
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4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
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24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2855	100.0	2856	22 AAD13444	Human interleukin-
2	2652	92.9	2725	24 ABL61567	Human interleukin
C 3	1178.8	41.3	32177	22 ABA18493	Human nervous syst
C 4	1178.8	41.3	32177	22 AAS29828	Human cytoskeletal
C 5	1178.8	41.3	32177	22 AAL05374	Human reproductive
6	1078	37.7	1827	22 AAD13443	Human interleukin-
7	1051.2	36.8	1701	21 AAB87757	Human secreted pro
8	1051.2	36.8	1701	21 AAF64039	cDNA encoding huma
9	1041.8	36.5	1796	22 AAS18126	Human DNAX cytokin

10	1040.2	36.4	1713	24 ABA03202	Human IL-17 recept
11	1040.2	36.4	1841	24 AAD28776	Human interleukin-
12	1040.2	36.4	1841	24 ABA03200	Human IL-17 recept
13	1040.2	36.4	2015	24 AAD28777	Human interleukin-
14	1040.2	36.4	2015	24 ABA03201	Human IL-17 recept
15	1039.6	36.4	2161	22 AAH99008	Human EST-derived
16	1038.6	36.4	1818	22 AAD12581	Human protein havi
17	1038.6	36.4	1918	21 AAA75772	cDNA encoding a hu
18	1038.6	36.4	1918	21 AAZ52046	cDNA encoding inte
19	1031.4	36.1	1816	21 AA75761	cDNA encoding a hu
20	1031.4	36.1	1816	21 AAZ52035	cDNA encoding inte
21	1031.4	36.1	1816	21 AAZ52035	Human interleukin
22	936.6	32.8	2080	21 AAA95789	Human immune syate
23	763.4	26.7	1515	22 AAS46124	Human DNA encoding
24	763.4	26.7	1515	22 AAS09514	Human cDNA encoding
25	763.4	26.7	1515	22 AAF92136	Human PRO5801 cDNA
26	559.4	19.6	714	20 AAZ08982	Human IL-17RH cDNA
27	551	19.3	1506	24 AAS18127	Human DCRS6 revers
28	498.6	17.5	1963	22 AAD13445	Mouse interleukin-
29	498.6	17.5	2589	22 AAD13446	Mouse interleukin-
C 30	451	15.8	603	24 ABQ59113	Human colon cancer
C 31	353.2	12.4	471	24 ABQ58257	Human colon cancer
32	331.6	11.6	405	22 AAF66413	Novel human polynu
33	329.8	11.5	397	22 AAF66470	Novel human polynu
34	326.4	11.4	409	21 AAA75762	cDNA clone sequenc
35	326.4	11.4	409	21 AAZ35747	HPCH63R cDNA clon
36	326.4	11.4	409	21 AAZ35747	Human interleukin
37	242.4	8.5	374	22 AAF98686	Human ovarian canc
38	205.4	7.2	218	16 AAT24669	Human gene signatu
39	182.6	6.4	327	21 AA75763	cDNA clone sequenc
40	182.6	6.4	327	21 AAZ52037	HETCC45RA cDNA clo
41	182.6	6.4	327	21 AAZ35748	Human interleukin
42	139.4	4.9	637	24 AAS18128	Mouse DNAX cytokin
C 43	114	4.0	116	19 AAX12137	Human biallelic po
44	108.8	3.8	210	24 AAS18129	Mouse DCRS6 revers
C 45	65	2.3	6694	24 ABL70352	Chemically treated

ALIGNMENTS

RESULT 1

AAD13444

ID AAD13444 standard; cDNA; 2856 BP.

AC AAD13444;

XX AAD13444;

DT 06-NOV-2001 (first entry)

XX Human interleukin-17 receptor related protein (Evi27) encoding cDNA #2.

DE Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21;

XX Evi27; retroviral integration; chromosomal mapping; mutational analysis;

KW BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy;

KW haematopoietic cell; cancer; autoimmune disease; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS

XX 6..872

XX /*tag= a

XX /product= "Human Evi27 protein"

XX WO200157202-A2.

PN 09-AUG-2001.

PD 02-FEB-2001; 2001WO-US03518.

XX 04-FEB-2000; 2000US-0180374.

XX (UYAR-) UNIV ARKANSAS.

XX

XX

XX

XX

XX

XX

XX

PI Shaughnessy JD;
 XX WPI; 2001-496920/54.
 DR P-PSDB; AAE07161.
 XX
 PT New nucleic acids encoding an interleukin (IL)-17 receptor related
 PT protein for use as a marker for leukemia -
 XX
 PS Claim 1a; Page 75-76; 87pp; English.
 XX
 CC The present sequence is a cDNA encoding human interleukin (IL)-17
 CC receptor related protein (Evi27). Human Evi27 gene was mapped to
 CC chromosome 3p21. Evi27 is a common site of retroviral integration
 CC in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful
 CC as antisense molecules to inhibit Evi27 protein or for chromosomal
 CC mapping or mutational analysis of Evi27 protein. They are proviral
 CC integration sites associated with leukaemias and monitoring this
 CC site provides a genetic tag for disease gene identification. The
 CC proteins of the invention are useful to stimulate the secretion of
 CC proinflammatory cytokines such as IL-8 and plays an important role
 CC in the developmental and/or disease processes of haematopoietic
 CC cells. Hence modulating the expression of Evi27 at the RNA or
 CC protein level is used in the treatment of diseases such as cancer
 CC or autoimmune diseases.
 XX
 SQ Sequence 2856 BP; 793 A; 655 C; 682 G; 725 T; 1 other;
 Query Match 100.0%; Score 2855; DB 22; Length 2856;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 181 CAGGGGACTATTCAATTTTGAATGTAATGTAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 240
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 DB 421 ATAATATCTTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 480
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Db 2821 TTCCAAAAA 2856

RESULT 2
ABL61567
ID ABL61567 standard; cDNA; 2725 BP.
AC ABL61567;
XX
XX
XX 20-SEP-2002 (first entry)
XX
DE Human interleukin receptor-ligand (IL-17B and IL17BR) 32.56 cDNA.
XX
XX Human interleukin receptor-ligand (IL-17B and IL17BR) 32.56;
KW rheumatoid arthritis; inflammation; immunological disease; tumour;
KW development disturbance; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1689..2579
XX FT /*tag= a
XX FT /product= "interleukin receptor-ligand (IL-17B and
XX IL17BR) 32.56"
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XX CN1341660-A.
XX
XX 27-MAR-2002.
XX
XX 07-SEP-2000; 2000CN-0125085.
XX
XX 07-SEP-2000; 2000CN-0125085.
XX
XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-520727/56.
XX P-PSDB; ABB84242.
XX
XX Novel human interleukin receptor-ligand (IL-17B and IL17BR) 32.56 -
XX
XX Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.
XX
XX This invention describes a novel human interleukin receptor-ligand
XX (IL-17B and IL17BR) 32.56. The product of the invention can be used to
XX treat several diseases, such as rheumatoid arthritis, inflammation,
XX immunological disease, various tumours and development disturbance. This
XX sequence encodes the human interleukin receptor-ligand (IL-17B and
XX IL17BR) 32.56 described in the method of the invention.
XX
XX SQ Sequence 2725 BP; 705 A; 649 C; 686 G; 685 T; 0 other;

Query Match 92.9%; Score 2652; DB 24; Length 2725;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2672; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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QY 121 ATCTAATCCCGGAGACTTTGAGGACCTCCGAGTAGAACCTTTCAACTAGTGTGCAA 180
Db 158 ATCTAATCCCGGAGACTTTGAGGACCTCCGAGTAGAACCTTTCAACTAGTGTGCAA 217
QY 181 CAGGGGACTTATCAATTTTGTATGTAAGCTGGGTACTCCGGGAGATGCCAGCATCC 240
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QY 481 CACAGGCTGCCCTAGACCACATATGAATATATAAAAAAGTGTGTCAAGGCCGGAAGCC 540
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QY 1861 TCCCTTTCCCTCTGGATAACAAACAAAGCAAGCCGGGAGGCTGGCTGCTCTCTCTCTGC 1920
Db 1897 TCCCTTTCCCTCTGGATAACAAACAAAGCAAGCCGGGAGGCTGGCTGCTCTCTCTCTGC 1956
QY 1921 TGTCTCTGTGTGGCCACATGGGTGCTGGTGGCAGGATCTATCTAATGTGGAGGACG 1980
Db 1957 TGTCTCTGTGTGGCCACATGGGTGCTGGTGGCAGGATCTATCTAATGTGGAGGACG 2016
QY 1981 AAAGATCAAGAGACTTCTTTTCTACCCACACTACTGCCCCCAATTAAGTGTCTTG 2040
Db 2017 AAAGATCAAGAGACTTCTCTTTTCTACCCACACTACTGCCCCCAATTAAGTGTCTTG 2076
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QY 2101 AAAACCATTTGCAGAGTGAAGTCACTCTTGAAGAGGCGAGAAAGAAATAGCAGAGA 2160
Db 2137 AAAACCATTTGCAGAGTGAAGTCACTCTTGAAGAGGCGAGAAAGAAATAGCAGAGA 2196
QY 2161 TGGGTCCAGTGCAGTGGCTTGCCTCAAAAGAGGCGAGACAAAGTCTTCTCTTC 2220
Db 2197 TGGGTCCAGTGCAGTGGCTTGCCTCAAAAGAGGCGAGACAAAGTCTTCTCTTC 2256
QY 2221 TTTTCAATGAACCTCAACAGTGTGCGATGTTGCTGCGAAGAGCGAGGCGAGTCCCA 2280
Db 2257 TTTTCAATGAACCTCAACAGTGTGCGATGTTGCTGCGAAGAGCGAGGCGAGTCCCA 2316
QY 2281 GTGAGAACTCTCAAGACCTTTTCCCTTGGCTTTAACTTTTCTGAGTGTATTAAGAA 2340
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 AC ABA18493;
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 DT 23-JAN-2002 (first entry)
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 DE Human nervous system related polynucleotide SEQ ID NO 10824.
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 KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antisickling; antianemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200159063-A2.
 XX
 PD 16-AUG-2001.
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 PF 17-JAN-2001; 2001WO-US01334.
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 PR 31-JAN-2000; 2000US-0179065.
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08-NOV-2000; 2000US-0246532.
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 06-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
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 08-DEC-2000; 2000US-0251989.
 08-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
 cancers and metastases -
 Disclosure; SEQ ID NO 10824; 1701pp + Sequence Listing; English.
 The invention relates to novel genes (AB11004-AB21534) and proteins
 (AB114678-AB218001) useful for preventing, treating or ameliorating
 medical conditions e.g. by protein or gene therapy. The genes are
 isolated from a range of human tissues disclosed in the specification.
 The nucleic acids, proteins, antibodies and (ant)agonists are useful
 in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 and ovarian cancer and other cancers of the adrenal gland, bone, bone
 marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 and parasitic infections.
 Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 32177 BP; 8826 A; 6801 C; 7130 G; 9420 T; 0 other;

Query Match 41.3%; Score 1178.8; DB 22; Length 32177;
 Best Local Similarity 98.0%; Pred. No. 4.7e-269;

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QY 663	TCCTCAGGTGTTT	GAGCCACAC	CAGAGAAACAAACG	CAGCTT	CAGTGTGATTTCCAGTG 722
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DB 24432	AAGGACATAGAA	GACTGTTCC	ATTCATTCAT	TGCTTT	TAAGATGAGTTCTCTTGTC 24373
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QY 963	AATGGCTGCTGA	CCCTTCAA	AAGCACTTT	TATTTAT	TCTTCTGTCAACACCTCAGG 1022
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QY 1383	TGGAGAACCAT	AGACTTCC	CTTACT	ACAGG	ACTTGCATGCTCTAAAGCAGTGGCTGAAG 1442
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QY 1563	GGTTCCAGAC	CCCCGG	GAGTCT	TGGG	CATGTTGGGTCTCGGGTCACTGCTTTTGTAGGG 1622
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QY 1623	CTTTGTTTCA	GATGTGTG	ACCAAG	GGGAA	AAATGTCATGACAACTAGAGTAGGGGG 1682
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OY 1863 CCTTCCCTCTCGATAACCAACAAAGC 1889
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DB 23353 CCTTCCCTCTCGATAACAGTAAGTCC 23327
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RESULT 4
ID AAS29828/c
ID AAS29828 standard; DNA; 32177 BP.
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DT 21-NOV-2001 (first entry)
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DE Human cytoskeletal element-related polypeptide encoding genomic DNA #15.
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KW Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse;
KW cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine infection;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility; food additive.
XX
OS Homo sapiens.
XX
PN WO200155169-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01331.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
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DT 21-NOV-2001 (first entry)
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DE Human reproductive system related antigen DNA SEQ ID NO: 8062.
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KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; Gene therapy; ds.
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
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PR 14-AUG-2000; 2000US-0225447.
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PR 21-DEC-1999; 99US-0469099.
 XX (GEST) GENSET.
 PA Dumas Milne Edwards J, Bougueleret L, Jobert S;
 PI WPI; 2001-071487/08.
 XX
 XX 49 Secreted proteins and the nucleic acids encoding them, useful in
 PT gene therapy and for detecting similar sequences in samples -
 XX
 PS Claim 1; Page 259-261; 307pp; English.
 XX
 CC The present invention relates to 49 Secreted proteins and the cDNAs
 CC encoding them. The protein and nucleic acids may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate protein expression.
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 XX Sequence 1701 BP; 499 A; 412 C; 372 G; 418 T; 0 other;
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 Best Local Similarity 99.2%; Pred. No. 2.8e-239;
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 AC AAS18126;
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 DT 26-MAR-2002 (first entry)
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 DE Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA.
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 KW Human; DNAX cytokine receptor subunit 6; DCRS6; phosphate labelling; ss;
 KW gene therapy; protein therapy; immunological disorder.
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 OS Homo sapiens.
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 PN WO200190358-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US16767.
 XX
 PR 24-MAY-2000; 2000US-206862P.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 PI Gorman DM;
 XX
 DR WPI; 2002-106198/14.
 DR P-PSDB; AAU11351.
 XX
 PT Isolated antigenic human or mouse DNAX receptor subunit-like
 PT polypeptide useful for detecting antibodies generated in response to
 PT presence of increased protein levels or immunological disorders -
 XX
 PS Disclosure; Page 7-10; 148pp; English.
 CC
 CC The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.

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DT	07-MAY-2002	(first entry)	
XX	XX		
DE	Human Interleukin-17 receptor B-2 (IL-17RB-2)	DNA.	
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KW	Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;		
KW	cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;		
KW	inflammatory bowel disease; neuronal dysfunction; transplant rejection;		
KW	autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;		
KW	infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;		
KW	cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;		
KW	eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;		
KW	epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;		
KW	leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;		
KW	cancer; diabetes; ds.		
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OS	Homo sapiens.		
XX	XX		
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PN	W0200208285-A2.		
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PD	31-JAN-2002.		
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PF	21-JUN-2001; 2001WO-US19861.		
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PR	22-JUN-2000; 2000US-213125P.		
PR	02-FEB-2001; 2001US-266159P.		
PR	16-MAR-2001; 2001US-0810384.		
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PA	(AMGB-) AMGEN INC.		
XX	XX		
PI	Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;		
XX	XX		
DR	WPI; 2002-155217/20.		
DR	P-PSDB; AAE18127.		
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PT	Nucleic acid molecules encoding Interleukin 17 (IL-17) - like		
PT	polypeptides useful in the treatment, prevention and diagnosis of		
PT	diseases e.g. cancer		
XX	XX		
PS	Disclosure; Page 230-232; 242pp; English.		
XX	XX		
CC	The invention relates to nucleic acid molecules encoding Interleukin 17		
CC	(IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels		
CC	of IL-17 protein in an animal. The IL-17 protein is useful for treating,		
CC	preventing or ameliorating a disease, such as immune system dysfunction		
CC	(rheumatoid arthritis, osteoarthritis, inflammatory joint disease);		
CC	autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel		
CC	disease, transplant rejection, graft vs. host disease); infections (HIV,		
CC	hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,		
CC	sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung		
CC	(acute respiratory distress syndrome, cystic fibrosis, emphysema); skin		

CC ischaemia), eye disorders, reproductive disorders, tumours and CC inflammation.

Query Match 36.4%; Score 1040.2; DB 24; Length 1841;
Best Local Similarity 99.7%; Pred. No. 1.2e-236;
Matches 1042; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy	1899	GGCTGGCTGCTCTCCTCTCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGTGGCAGGG	1958
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Qy	2559	CAAGAGACCTTAAAGCTTCCATCCACCAATTACAGGAAAAAAAGTGTGATGATCTCT	2618
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DT	07-MAY-2002 (first entry)
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DE	Human Interleukin-17 receptor B-3 (IL-17RB-3) DNA.

Human; interleukin-17 receptor B-3; IL-17RB-3; immune system dysfunction;
 cystic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
 inflammatory bowel disease; neuronal dysfunction; transplant rejection;
 autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
 infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
 cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
 eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
 epilepsy; atherosclerosis; heart failure; angiodenesis; endometriosis;
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 cancer; diabetes; ds.

XX Homo sapiens.

Key	Location/Qualifiers
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FT	50..92
FT	/tag= b
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FT	/product= "Mature IL-17RB-3 protein"

WO200208285-A2.

31-JAN-2002.

21-JUN-2001: 2001WO-US19861.

22-JUN-2000: 2000US-213125P.

02-FEB-2001; 2001US-266159P;
16-MAR-2001; 2001US-0810384;

(AMGE-) AMGEN INC.

Medlock E, Yeh R, Silbiger SM, Elliot GS, Nauven HO, Jing S:

WPI: 2002-155217/20.

P-PSDB; AAE18128.

nucleic acid molecules encoding interleukin 1/ (IL-1/), - like polypeptides useful in the treatment, prevention and diagnosis of diseases e.g. cancer -

Disclosure: Page 234-236: 242pp: English:

The invention relates to nucleic acid molecules encoding interleukin 17 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels of IL-17 protein in an animal. The IL-17 protein is useful for treating, preventing or ameliorating a disease, such as immune system dysfunction (rheumatoid arthritis, osteoarthritis, inflammatory joint disease); autoimmune arthritis, osteoarthritis, lupus, diabetes, inflammatory bowel autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel disease), transplant rejection, graft vs. host disease; infections (HIV, hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia, cachexia).

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:37:09 ; Search time 7273.44 Seconds
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1178.8	41.3	177072	9	AC012467	AC012467 Homo sapi
4	1078	37.7	1828	9	AF208110	AF208110 Homo sapi
5	1051.2	36.8	1701	6	AX061651	AX061651 Sequence
6	1041.8	36.5	1796	6	AX350967	AX350967 Sequence
7	1040.2	36.4	1713	6	AX253209	AX253209 Sequence
8	1040.2	36.4	1841	6	AX253204	AX253204 Sequence
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17	763.4	26.7	1515	6	AX092426	AX092426 Sequence
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31	101	3.5	2584	9	AK095091	AK095091 Homo sapi
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ALIGNMENTS

RESULT 1
AF208111

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AF208111 2856 bp mRNA linear PRI 17-JUL-2000
Homo sapiens truncated IL-17 receptor homolog precursor (EVI27)
mRNA, complete cds.

AF208111 GI:9246434

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2856)

Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.

and Shaughnessy, J.D. Jr.

TITLE Evi27 encodes a novel membrane protein with homology to the IL17 receptor

JOURNAL Oncogene 19 (17), 2098-2109 (2000)

MEDLINE 20273223

PUBMED 10815801

REFERENCE 2 (bases 1 to 2856)

AUTHORS Shaughnessy, J.D. Jr.

TITLE Direct Submission

JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W. Markham St., Little Rock, AR 72212, USA

FEATURES

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CDS

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/note="lacks transmembrane and cytoplasmic domains"

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/note="putative; glycosylation site"

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/note="unspliced intron in this isoform"

polya_signal

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/gene="EVI27"

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 ATAATATTCTTAATGCAATATGAATGAAGTGGCCCTTCCATGCTGTGTAATTTCACT 480

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DB 481 CACCAAGGCTGCTAGACACACATAATGAAATATAAAAAAGTGTCTCAAGGCCGGAAGCC 540

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RESULT 2
AC113172/c
LOCUS AC113172 149634 bp DNA linear PRI 31-JUL-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-739J4, complete sequence.
ACCESSION AC113172
VERSION AC113172.2 GI:22024573
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 149634)
AUTHORS Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E. D.
Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 149634)
AUTHORS Kaul, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.
Direct Submission
JOURNAL Submitted (26-FEB-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 149634)
AUTHORS Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E. D.
Direct Submission
JOURNAL Submitted (31-JUL-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Jul 31, 2002 this sequence version replaced gi:18921343.
----- Genome Center
Center: University of Washington
Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwchgts@u.washington.edu

----- Project Information

Center project name: chr-3

Center clone name: RP11-739J4 (bc0790)

----- Summary Statistics

Sequencing vector: plasmid; 100% of reads

Chemistry: Dye-terminator ET; 57% of reads

Chemistry: Dye-terminator Big Dye; 43% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 149509 bases at least Q40

Consensus quality: 149632 bases at least Q30

Consensus quality: 149634 bases at least Q20

Insert size: 149634; sum-of-contigs

Quality coverage: 8.9x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-126H24 (UWGC:bc0241) AC027471

3': RP11-884K10 (UWGC:bc0575) AC012467

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

EcoRI				HindIII				BglII			
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1476	1536	512	<800	6280	6434						
4410	4453	449	<800	160	<800						
589	<800	3754	3833	12532	12654						
1519	1536	2481	2481	12015	11825						
688	<800	2767	2826	8227	8201						
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6444	6507	481	<800	2999	3075						

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2454	2450	9111	9164	9252	9096
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2577	2577	303	<800	700	<800
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Matches 1203; Conservative 0; Mismatches 23; Indels 1; Gaps 1;			
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Qy	723	ACTGGGATAGTGAAGGTGCTACGGTGCAGGTAAAGTTTCAGTGAGCTGCTCTGGGAGGG	782
Db	137853	ACTGGGATAGTGAAGGTGCTACGGTGCAGGTAAAGTTTCAGTGAGCTGCTCTGGGAGGG	137794
Qy	783	AAGGACATAGAGACTGTTCCATCATCTTCAATTCATTTTAAAGATGAGTTCTCTTTGTCA	842
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Qy	843	AATGCACCTCTGCGACGACACACAGTAAAGTTCAGTGGGCTTCATGGGGTCTTTTCGTCGAG	902
Db	137733	AATGCACCTCTGCGACGACACACAGTAAAGTTCAGTGGGCTTCATGGGGTCTTTTCGTCGAG	137674
Qy	903	CCTCCACCGTGTGAGGTGAGGAGCGGAGTGGCGAGTTGTGTCCTCTTTTGTGTATT	962
Db	137673	CCTCCACCGTGTGAGGTGAGGAGCGGAGTGGCGAGTTGTGTCCTCTTTTGTGTATT	137614
Qy	963	AATGGTGTGACCTTCCAAAGACATTTTATTTTATTTTCTGTCACAGACTCAGG	1022
Db	137613	AATGGTGTGACCTTCCAAAGACATTTTATTTTATTTTCTGTCACAGACTCAGG	137554
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Db	137493	GAATGGGAGGTTTTCAGTTCACGAGCGGTATGAACCTCTGGAGAGGGGCTGCCAGTCT	137434
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Db	137074	GATATGACCTAGCCCTTTTTCAGTAAAGCAACCTGGTATGTTAGTAACTGTACAAAGTTTA	137015
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Db	137014	GGTTCAGACCCCGGGAGTCTTCGGGCATGTGGGTCTCGGGTCACTGGTTTTGACATTTAGGG	136955
Qy	1623	CTTTGTTACAGATGCTGTACCAAGGGGAAATGTGCATGACAACTAGAGGTATGGGCG	1682
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ACCESSION	AC012467		
VERSION	AC012467.9 GI:7363385		
KEYWORDS	HTG.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 177072)		
AUTHORS	Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K., Bodota,B., Bouch,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,Y., Fernandez,C., Fennell,N., Dugan-Rocha,S., Durbin,K.J., Hernandez,C., Ferraguto,D., Forcum-Tansey,J., Frantz,P., Ganesh,R., Garcia,D.K., Gorrell,J.H., Gorrell,L.B., Guevara,W., Harris,K., He,X., Hernandez,J., Hodgson,A., Hogue,M., Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondeljewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,H., Shen,H., Simon,M., Sparks,A., Stamps,A., Suggang,R., Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wabbah,M., Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R. Unpublished		
TITLE	Direct Submission		
JOURNAL	Unpublished		
AUTHORS	Worley,K.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		

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DEFINITION	Homo sapiens chr3 BAC RP11-884K10 (Roswell Park Cancer Institute Human BAC Library) complete sequence.			
ACCESSION	AC012467			
VERSION	AC012467.9	GI:7363385		
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SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
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AUTHORS	Muzny D.M., Adams C., Bailey M., Barbara J., Blankenburg K., Bodota B., Bouck J., Bowie S., Brooks A., Buhay C., Bunac C., Burkett C., Burrows J., Carter M., Chacko J., Chen Z., Cox C., David R., Delgado O., Deshazo D., Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C., Ferraguto D., Forcun-Tansey J., Frantz P., Ganesh R., Garcia D.K., Gorrell J.H., Gorrell L.L., Guevara W., Harris K., He X., Hernandez J., Hodgson A., Hognes M., Holloway C., Hosak H., Jackson L.B., Jackson L., Jia Y., Jones M., Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichtarge O., Liu J., Liu W., Logan O., Lozado R.J., Lu J., Lucier R., Martin R., Martinez C., McLeod M.P., Mei G., Moore S., Moorish T., Morgan M., Morris S., Nash S., Nelson A., Nguyen R., Nguyen N., Nguyen S., Oswal G., Parish B., Paxton S., Payton B., Perez L., Pu L.L., Quiles M., Reiter D., Rives M., Samuel S., Say J., Scherer S., Shah E., Shen H., Simon M., Sparks A., Stamps A., Sugchang R., Tabor P., Taylor T., Vasquez L., Vinson R., Vo Q., Wabba M., Watlington S., Weinstein G., Weinstein I.R., Williamson A., Worley K., Wren J., Wrenford G., Yu W., Zhou X., Naylor S.L., Nelson D. and Gibbs R.			
TITLE	Direct Submission			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 177072)			
AUTHORS	Worley K.C.			
JOURNAL	Direct Submission			
TITLE	Submitted (28-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			

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 VERSION AF208110.1 GI:9246432
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 TIAN, E., SAWYER, J.R., LARGAESPAD, D.A., JENKINS, N.A., COPELAND, N.G.
 and SHAUGHNESSY, J.D., JR.
 EVI27 encodes a novel membrane protein with homology to the IL17
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 JOURNAL Oncogene 19 (17), 2098-2109 (2000)
 MEDLINE 20273223
 PUBMED 10815801
 REFERENCE 2 (bases 1 to 1828)
 AUTHORS Shaughnessy, J.D. Jr.
 TITLE Direct Submission
 JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research
 Center, University of Arkansas for Medical Sciences, 4301 W.
 Markham St., Little Rock, AR 72212, USA
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VERSION AX061651.1 GI:12406761
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REFERENCE 1. (bases 1 to 1701)
AUTHORS dumas mine Edwards, J.B., Bougueleret, L. and Jobert, S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 56 04-JAN-2001;
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ACCESSION AX253204
VERSION AX253204.1 GI:15986346
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REFERENCE 1 (bases 1 to 1841)
AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
Nguyen,H.Q.
TITLE IL-17 receptor like molecules and uses thereof
JOURNAL Patent: WO 0168705-A 1 20-SEP-2001;
Amgen Inc. (US)
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REFERENCE	1 (bases 1 to 2015)				
AUTHORS	Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and Nguyen,H.Q.				
TITLE	Il-17 receptor like molecules and uses thereof				
JOURNAL	Patent: WO 0168705-A 4 20-SEP-2001;				
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and
Jing, S.
TITLE 11-17 molecules and uses thereof
JOURNAL Patent: WO 0208285-A 19 31-JAN-2002;
Amgen, Inc. (US)
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ACCESSION BC000980
VERSION BC000980.1 GI:12654318
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REFERENCE 1 (bases 1 to 2042)
AUTHORS Strausberg, R.
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JOURNAL Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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Contact: villalob@bcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
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VERSION AX191534.1 GI:15209721
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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1818)
Kato,S. and Kimura,T.
TITLE Human proteins having hydrophobic domains and dnas encoding these
proteins
JOURNAL Patent: WO 0149728-A 56 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
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Best Local Similarity 99.6%; Pred. No. 2.3e-258;
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RESULT 15
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complete cds.
ACCESSION AF250309
VERSION   AF250309.1 GI:13649476
KEYWORDS  .
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1 (bases 1 to 1583)
           Zhang, W. and Cao, X.
           Direct Submission
           Submitted (29-MAR-2000) Department of Immunology, Second Military
           Medical University & Shanghai Brilliance Biotechnology Institute,
           800 Xiangyin Rd., Shanghai 200433, P.R. China
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic -- nucleic search, using sw model

Run on: May 27, 2003, 23:21:54 ; Search time 2725.67 Seconds
(without alignments)
11663.832 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum Match 0%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	624	31.8	678	10	BB307800 BB307800
5	554.8	28.3	646	10	BB644125 BB644125
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18	352.6	18.0	788	13	BI458542
19	352.2	17.9	523	10	BB284760
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ALIGNMENTS

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DEFINITION 602887278F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:504246
5', mRNA sequence.
ACCESSION BI103740
VERSION BI103740.1 GI:14554633
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Location/Qualifiers

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BB653710
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DEFINITION BB653710 RIKEN full-length enriched, adult male liver tumor Mus
musculus cDNA clone C730019M05 5', mRNA sequence.
ACCESSION BB653710
VERSION BB653710.1 GI:16487538
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 710)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1. 710
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
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GAGAGAGAGAGCGCGCGCAACTCGAGTTTTTTTTTTTTTTTTTTTNN 3'], cDNA was

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5].
GAGAGAGATTCGAGCTTAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge."

BASE COUNT 193 a 178 c 184 g 154 t 1 others
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 477 GTCTGTGAACCTTCACTCGCCAGGCTGCCTAAACACGTAATGAATATAAAGAGCTG 536
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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602 GGTGAAGTGAATTTCAACACCAATCCCTTGGAAACAGATACAGATCTCATTTCAAG 661
Qy 657 GGACACGACA-TTGGGGTCTTCTAGAGTCTCGAGATAA 695
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662 GGACACGACATTTGGGGGTTCTTAGAGTCTCGAGATAA 701

RESULT 3
BB667509 BB667509 728 bp mRNA linear EST 24-OCT-2001
LOCUS BB667509 RIKEN full-length enriched, adult male liver tumor Mus
DEFINITION musculus cDNA clone C730019M05 3', mRNA sequence.
ACCESSION BB667509

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

BB667509.1 GI:16398958
EST.
house mouse.
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 728)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Iehi, Y., Ito, M., Kawai, J., Kawai, J., Kondo, H., Kouda
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-rsg@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1. 728
/organism="Mus musculus"
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5].
GAGAGAGAGCGGCGCACTTTCAGTGTGCTCTGAGACAGGGCCATCTCCAGAGTGG
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5].


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Best Local Similarity 99.6%; Pred. No. 2e-101;
Matches 556; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGGCAGTGGCGGCGCATGTTGCTAGTGTCTGCTATCTTGGCTGCATCGTCAGGAGC 60
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Qy 301 AATTCTACAGTGTGTAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCAAGACT 360
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Qy 541 GAGGGCGGAAGCTGTGG 558
Db 629 GAGGGCGGAAGCTGTGG 646

RESULT 6
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LOCUS AL535617 LTI FL013_Fbrn1 Homo sapiens cDNA clone CS0DF016YG03 5
DEFINITION prime, mRNA sequence.
ACCESSION AL535617
VERSION AL535617.1 GI:12799110
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS Li W.B., Gruber, C., Jessee, J. and Pollayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMWSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 240 a 210 c 208 g 191 t 20 others
ORIGIN
Query Match 25.9%; Score 508.2; DB 9; Length 869;
Best Local Similarity 76.0%; Pred. No. 4.2e-92;
Matches 659; Conservative 17; Mismatches 175; Indels 16; Gaps 4;

Qy 15 GGCCAGTGTGCTAGTGTGCTGATCTTGGCTGCATCGTCAGAGGCGCCCTGCTCGAGAG 74
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Qy 75 GCGCAGTATTGCTGCTGCTGCTGAGACAGGGCCATCTCCAGAGTGGATGGTCCACACAC 134
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Qy 369 CAATGGACATCTCTCTATGAGGCTTCCCTGTGGAGTGGAGCTCTCTAT -CTCATCA 427
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Qy 488 TCACCTCGCCAGGCTGCTTAAACCAACGTAATGAATATAAAAGCAGTGCATCGAGCGG 547
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Qy 548 GAAGCTGTGGGAGCCGAGACATCTGCTTCTTAAAGAGAGAGAGATGTTGAAGTGA 607
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Qy 779 GCGGCAATGACTGCTCGAGCGGAGGAGCAGTGTGCTTTGCTCAGAGACAGAGTGTCT 838
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

MGI:1453973
Seq primer: -40UP from Gibco
High quality sequence stop: 367.

FEATURES
SOURCE

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Technologies."

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Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dbb 371 GGGAGAACTCTCAGGATCTGTCCCTCTTGCTTAACTCTTTTGTAAGTGAATTCAGCA 312

QY 1316 GCCAGAGCATGCGACAAATACCTGGTGTATCTTGGGGAGCAGACCTCAAGCG 1375

QY 1376 ACTATAATGCCCTGAGTGTCTGCCCCAAATCATCTCATGAAGGACGCCACAGCTTTC 1435

Db 251 ACTATAATGCCCTGAGTGTGCCCCCAATATCATCTCATGAAGGACGCCACAGTTTCC 192

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Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 425)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and
Waterson, R.

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Research	1980, Vol. 83, No. 2, pp. 11-20
3. The Importance of Parental Involvement	Journal of Educational Research	1980, Vol. 83, No. 3, pp. 21-30
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 4, pp. 31-40
5. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 5, pp. 41-50
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 6, pp. 51-60
7. The Importance of Teacher Evaluation	Journal of Educational Research	1980, Vol. 83, No. 7, pp. 61-70
8. The Effect of Teacher Salary on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 8, pp. 71-80
9. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 9, pp. 81-90
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 10, pp. 91-100

Contact: Maria Wyomuse ESI Project
 WashU-HHMI Mouse ESI Project
 Washington University School of
 4444 Forest Park Parkway, Box 850
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseesi@watson.wustl.edu
 This clone is available royalty-free to
 IMAGE Consortium (info@image.llnl.gov)
 MGI: 694245
 Seq primer: -28ml3 rev2 ET from A
 Seq primer: -28ml3 rev2 ET from A
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 In-house quality stop: 402.

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TGTTACCAATCTGAAGTGGAGCGCGCGTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
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provided by Dr. Bertrand Jordan. Library went through two  
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Soares and M.Fatima Bonaldo."  
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DD

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Qy 534 GTCACTAGGCGGAGCTGTGGAGCCAGACATCACTGCTTGTAAAGAACAGAA 593
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Qy 594 GATGGTGAAGTGAATTTCAACACCAATCCCTTGAACACAGATACACATCTCATTC 653
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DEFINITION 303426 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG384365
VERSION BG384365.1 GI:13308837
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980504.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT

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Best Local Similarity 81.4%; Pred. No. 1.3e-66;
Matches 442; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 1 GTGGCCAGTGGCCGGCCATGTTGCTAGTGTGCTGATCTTTGGGTGCTATCGTGACAGGAGC 60
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Db 429 TTCATTTGAGGCCCAATATATCCCAATGCAATATGAACGAAGATGGCCCTCTCTTGGCT 488
Qy 481 GTGAATTCACCTCGCAGGCTGCTAAACCAACGCTAATGAATATAAAGCAGTGCAT 540
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Qy 541 GAG 543
Db 549 GAG 551

RESULT 13
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DEFINITION 388904 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI360842
VERSION BI360842.1 GI:15056870
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 588)

```

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

JOURNAL Unpublished (2000)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 141 row: I column: 23
Seq primer: ATTAGGTGACACTATAG.

FEATURES
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/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 146 a 151 c 165 g 126 t

ORIGIN
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Best Local Similarity 81.2%; Pred. No. 4.4e-66;
Matches 440; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 1 GTGGCCAGTGGCGGGCCATGTTGCTAGTGTCTGCTGATCTTGCTGCATCGTCGAGAGC 60
DB |||||
DB 47 GCGGGAAGTCGCCCGCGATGTTACTAGTGTCTGCTGAGCGTGGCCGCTGCTGGGT 106
QY 61 GCCTGCTCGAGAGCGGACTTACGTGCTGCTGCTGAGCAGGGCCACTCCAGAGTGG 120
DB |||||
DB 107 GCATGCTCCAGAGCGGACAATTCAGTGTGCTGCTGAGCCTGAGTGTCCAGAAATGG 166
QY 121 ATGGTCCAAACACACACTCACTCAGAGAGACTTGAGGAGCTCCAACTGGAACCTCGTCAAG 180
DB |||||
DB 167 ATGGGTGACACCGCTCTGACCCAGAGACTTGAGGGACTCCGAGTGGAACTATTAA 226
QY 181 ACAAGTGGCGAGCAGAGAGTTTCAATTTGATGAAATAGCTGGATACTCCGGCA 240
DB |||||
DB 227 AGCAGTGTTCAGTGGAGGACTATTCAATTTTGATGAACATAAGCTGGATACTCCGGCA 286
QY 241 GACGCCAGATCGCTTGTGAGGCGCCACAGATCTGGTGTGGGCAAAACACATG 300
DB |||||
DB 287 GATGCCAGTATCGATGTTGTAAGGCCACCAAGATCTGTGTGACGGCGAAGCCAGAG 346
QY 301 AATTATACAGCTGTGTGAGTGCAACTACACAGAGCGCTTCCAAAGCCAGACCACT 360
DB |||||
DB 347 CAGACCTACAGCTGTGTGAGTGCATTACACTGAGGCTTCCAGACTCAGACCACT 406
QY 361 TCGGCGGCAATGGACATCTCTATAGGCTTCCCTGTGGAGCTGAGCACTCTCTAT 420
DB |||||
DB 407 TCTGGCGGCAATGGATGTTTCTACGTAGGCTTCCAGTAGAGCTGAATACAGCTAT 466
QY 421 CTCATCAGCGCCATACATCCCAATGCTATATGAATGAGACAGCCCTCTTGTCT 480
DB |||||
DB 467 TTCAITGGAGCCCATATATCCCAATGCAATATGAACCAAGATGGCCCTCTTGGCT 526
QY 481 GTGAACCTCCACCTCGCAGGCTGCCTAAACACAGTAAATGAAATATAAAAGCAGTCACT 540
DB |||||
DB 527 GTGAACCTCACCTCACCAGGCTGCCTGGACCGCATTAATGAATACAAAAGATGCATT 586

QY 541 GA 542
DB 587 GA 588

RESULT 14
LOCUS AAS62342
DEFINITION V122H03.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:973013 5', mRNA sequence.

ACCESSION AAS62342
VERSION AAS62342.1 GI:2333807
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 370)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMT Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMT Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:553741

Putative full length read
vector to vector length is 377
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 326.

FEATURES
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/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: phuescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'."

BASE COUNT 105 a 73 c 91 g 101 t

ORIGIN
Query Match 18.7%; Score 366.8; DB 9; Length 370;
Best Local Similarity 99.5%; Pred. No. 1.3e-63;
Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 GACTCTGAAATGTGGGAGAGGCTGTGTGGAGGTAGTGTATGTACAACTTGCTTTAA 1645
DB 1 GACTCTGAAATGTGGGAGAGGCTGTGTGGAGGTAGTGTATGTACAACTTGCTTTAA 60

QY 1646 PACTGGATTTGCAAGTCACCTGAGCATACACCGCTGAGGCTAGTCACTTGGCTGGATT 1705
DB |||||

QY 61 AACTGGATTTGCAAGTCAACCTGAGCATACACCGCTGAGGCTAGTCACTTGGCTGGATT 120
DB |||||

QY 1706 TATGAAGCAACACAGTGTACAGACAATAATAGTGGGACCTACATTGGGATATACCCAA 1765
DB |||||

QY 121 TATGAAGCAACACAGTGTACAGACAATAATAGTGGGACCTACATTGGGATATACCCAA 180
DB |||||

QY 1766 AGCTGGGTAAATGATTATCATCTGAGAACCAACGCACTCTGGCCATGAAGTAATACGGCACTT 1825
DB |||||

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Db 181 AGCTGGTAATGATATCACTGAGAACACGCACTCTGGCCATCAGGTAATACGGCACTT 240
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Db 241 CCCTGTCCAGGCTCTGTCTAGGTTGGTCTCTTGCACATGCCCATGCTCTATGCTGCAC 300
Qy 1886 GTAGACCGTTTGTGTAACATTTTAATCTGTTAAATGAATAATCCGTTTGGGAAGCTCTCAAA 1945
Db 301 GTAGACCGTTTGTGTAACATTTTAATCTGTTAAATGAATAATCCGTTTGGGAAGCTCTCAAA 360
Qy 1946 AAAAAAAAAA 1955
Db 361 AAAAAAAAAA 370

RESULT 15
BM693867
LOCUS
DEFINITION
  UI-E-DWI-ahc-i-22-0-UI.t1 UI-E-DWI Homo sapiens cDNA clone
  UI-E-DWI-ahc-i-22-0-UI 5', mRNA sequence.
ACCESSION
  BM693867
VERSION
  BM693867.1 GI:19007125
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 652)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  Contact: Soares, MB
  Program for Rat Gene Discovery and Mapping
  University of Iowa
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: msoares@blue.weeg.uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
  Location/Qualifiers
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      /db_xref="taxon:9606"
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      /clone_lib="UI-E-DWI"
      /tissue_type="lens"
      /dev_stage="adult"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /note="organ: eye; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site_1: EcoR I; Site_2: Not I;
      UI-E-DWI is a normalized cDNA library containing the
      following tissue(s): lens. The library was constructed
      according to Bonaldo, Lennon and Soares, Genome Research,
      6:791-806, 1996. First strand cDNA synthesis was primed
      with an oligo-dT primer containing a Not I site. Double
      stranded cDNA was ligated to an EcoR I adaptor, digested
      with Not I, and cloned directionally into pT73-Pac
      vector. The oligonucleotide used to prime the synthesis of
      first-strand cDNA contains a library tag sequence that is
      located between the Not I site and the (dT)18 tail. The
      sequence tag for this library is CGATTAGCGA. This library
      was created for the program, Gene Discovery in the Visual
      System, supported by National Eye Institute (NEI)."
    188 a 167 c 135 g 162 t
  
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ORIGIN

Query Match 18.6%; Score 366; DB 14; Length 652;

Best Local Similarity 76.0%; Pred. No. 1.6e-63;

Matches 465; Conservative 0; Mismatches 145; Indels 2; Gaps 1;

Qy 965 AGACGTCTCTTTCTCTATTTCCACCATCTCTCCCTCATTAAGGTCCTGTGGTTTATC 1024

Db 1 AGAAGACTCTCTTTTCTACCAACACACTACTGCCCCCATTAAGGTTCTGTGGTTTACC 60

Qy 1025 CTTCTGAGATATGTTTTCATCAACCGTCTGCGTCTCACTGACTTCTTCAAAACTACT 1084

Db 61 CATCTGAATATGTTTCCATCACACAAATTTGTTACTTCACTGAAATTTCTTCAAAACCAT 120

Qy 1085 GCAGAAGTCAGGTCACTCTTGAATAATGCAGAAAAGAAATCCCGAGATGGGGCCGG 1144

Db 121 GCAGAAGTCAGGTCACTCTTGAATAATGCAGAAAAGAAATAGCAGAGATGGGTCCAG 180

Qy 1145 TACAGTGGCTGACCACTCTCAGAAAGCAAGCGGCAGATAAAGTGGTCTTCTTCCAGTG 1204

Db 181 TGCAGTGGCTTGGCACTCAAAAGAGGCGAGACAAAGTCGTCTTCTTCTTCCCAATG 240

Qy 1205 AGTCCCGACCTTTGTGACAGTGCCTGTGGCCACAATGAGGGCAGCGCCAGGAGAACT 1264

Db 241 ACGTCAACAGTGTGTGCGATGTGTCTGTGGCAAGAGCGAGGGCGATCCCACTGAGA 300

Qy 1265 CTCAGGATCTGTCCCTCTTGCCTTTAACTCTTTTGTAGTGAATTCAGCAGCCAGACGC 1324

Db 301 CTCAGGATCTGTCCCTCTTGCCTTTAACTCTTTTGTAGTGAATTCAGCAGCCAGATTC 360

Qy 1325 APTCTGCACAAATFACCTGGTGGTCTATCTTGGGGGAGCAGACCTCAAAGCGCACTATAATG 1384

Db 361 ATCTGCACAAATFACCTGGTGGTCTATCTTGGGGGAGCAGATTTAGATACAAAGACGATTA 420

Qy 1385 CCTGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCCACAGCTTTCCACAGAAC 1444

Db 421 CTCTCAGTGTCTGCCCCCAAGTACCACCTCATGAAGGATGCCACTCTTCTGTGCGAGAAC 480

Qy 1445 TTCTCAAGCTACGAGAGCATGTCTAGTGAAGAAAGCTCACAAGCCTGCCATGATAGCT 1504

Db 481 TTCTCCATGTCAAGCAGCAGGTGTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540

Qy 1505 GTTCAACCTTGTAGTCCACCCCGGGGAAA--TAGAGACTCTGAAGCCTTCTTACTCTCCCT 1562

Db 541 GCTGCTCTTGTAGCCCAACCCCATGAGAGCAAGACCTTAAAGGCTTCTTATCCACCA 600

Qy 1563 TCCAGTGACAAA 1574

Db 601 ATTACAGGGAAA 612

Search completed: May 28, 2003, 10:13:27

Job time : 2742.92 secs

FEATURES

source

BASE COUNT

GenCore version 5.1.4_p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:34:39 ; Search time 220.213 Seconds
(without alignments)
11770.723 Million cell updates/sec

Title: US-09-778-971-3
Perfect score: 1963
Sequence: 1 gggccagtggccggccat.....aaaaaaaaaaaaaaaaaa 1963

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1472.2	75.0	2589	10	US-09-778-971-4
3	988.2	50.3	1841	10	US-09-886-404-17
4	983	50.1	1796	9	US-09-863-818A-1
5	980.8	50.0	1827	10	US-09-778-971-1
6	963.6	49.1	1515	9	US-09-874-503-11
7	963.6	49.1	1515	9	US-10-000-157-11
8	963.6	49.1	1515	9	US-10-063-547-157
9	963.6	49.1	1515	9	US-09-747-259-11
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15	963.6	49.1	1515	9	US-10-173-706-399
16	963.6	49.1	1515	9	US-10-173-738-399
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18	963.6	49.1	1515	9	US-10-176-482-399
19	963.6	49.1	1515	9	US-10-176-757-399

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21	963.6	49.1	1515	9	US-10-180-552-399	Sequence 399, App
22	963.6	49.1	1515	9	US-10-180-557-399	Sequence 399, App
23	963.6	49.1	1515	9	US-10-173-700-399	Sequence 399, App
24	963.6	49.1	1515	9	US-10-174-572-399	Sequence 399, App
25	963.6	49.1	1515	9	US-10-174-579-399	Sequence 399, App
26	963.6	49.1	1515	9	US-10-174-582-399	Sequence 399, App
27	963.6	49.1	1515	9	US-10-174-588-399	Sequence 399, App
28	963.6	49.1	1515	9	US-10-175-739-399	Sequence 399, App
29	963.6	49.1	1515	9	US-10-175-740-399	Sequence 399, App
30	963.6	49.1	1515	9	US-10-175-743-399	Sequence 399, App
31	963.6	49.1	1515	9	US-10-176-488-399	Sequence 399, App
32	963.6	49.1	1515	9	US-10-176-492-399	Sequence 399, App
33	963.6	49.1	1515	9	US-10-176-747-399	Sequence 399, App
34	963.6	49.1	1515	9	US-10-176-750-399	Sequence 399, App
35	963.6	49.1	1515	9	US-10-176-985-399	Sequence 399, App
36	963.6	49.1	1515	9	US-10-176-987-399	Sequence 399, App
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39	963.6	49.1	1515	9	US-10-176-993-399	Sequence 399, App
40	963.6	49.1	1515	9	US-10-184-658-399	Sequence 399, App
41	963.6	49.1	1515	9	US-10-173-695-399	Sequence 399, App
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ALIGNMENTS

RESULT 1
US-09-778-971-3
; Sequence 3, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: prim transcript
; OTHER INFORMATION: cdna of mouse Evi27
US-09-778-971-3

Query Match	100.0%	Score 1963;	DB 10;	Length 1963;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1963;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTGGCCAGTGGCCGGCCCATGTTGCTAGTGTGCTGATCTTGGCTGCATCGTGCAGGAGC	60	
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Qy	61	GCCTTCGCTCGAGAGCCGCACTATTTCAGTGTGGCTCTGAGACAGGGCCCATCTCCAGAGTGG	120	
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Qy	121	ATGGTCCAAACACACTCACTCCAGAGACTTGGAGGACCTCCAAAGTGAATCTCTCAAG	180	
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QY 607 AATTTTCAACCAATCCCTTTGGAAACAGATACAGGATCTCTATTCAACGGGACACGACA 666
Db 1233 AATTTTCAACCAATCCCTTTGGAAACAGATACAGGATCTCTATTCAACGGGACACGACA 1292
QY 667 TTGGGGTTTTCTAGAGTGTCTGGAGATAAATCTGATGAGGACGCTCTGTAGCCATCCCGGTG 726
Db 1293 TTGGGGTTTTCTAGAGTGTCTGGAGATAAATCTGATGAGGACGCTCTGTAGCCATCCCGGTG 1352
QY 727 ACTGAGAGAGTGAAGTGGCGGTGGTTTCACTGACGCCCATATTTATACATCTCGGGCAAT 786
Db 1353 ACTGAGGAGAGTGAAGTGGCGGTGGTTTCACTGACGCCCATATTTATACATCTCGGGCAAT 1412
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Db 1413 GACTGCATCCGACCGAAGGGACAGTTGTGCTTTTGTCTGAGACAAAGTGTCTCCATCCCT 1472
QY 847 CCAGATGACAAACAGACGATGCTGGGAGGCTGGCTGCTCTCTTCTGCTGCTGCTGGTG 906
Db 1473 CCAGATGACAAACAGACGATGCTGGGAGGCTGGCTGCTCTCTTCTGCTGCTGCTGGTG 1532
QY 907 GCTGTGTGGTGTGGGAGCTGGGATCTACTAACTTTGGAGGCAAGAGGACGACGAAG 966
Db 1533 GCTGTGTGGTGTGGGAGCTGGGATCTACTAACTTTGGAGGCAAGAGGAGGACGACGAAG 1592
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QY 1087 AGAAGTGAGTATCTTTGAAAATGCGAGAAAAGAAAATCCCGAGATGGGCGCGGTA 1146
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QY 1267 CAGGATCTGTTCCTCTTGCCTTTAACTCTTTTGTAGTGAATTCAGCAGCCAGCGCAT 1326
Db 1893 CAGGATCTGTTCCTCTTGCCTTTAACTCTTTTGTAGTGAATTCAGCAGCCAGCGCAT 1952
QY 1327 CTGCAAAATACCTGTGTCTATCTTGGGGAGCAGACTCTCAAGGCGACTATATGCC 1386
Db 1953 CTGCAAAATACCTGTGTGTCTATCTTGGGGAGCAGACTCTCAAGGCGACTATATATGCC 2012
QY 1387 CTGAGTGTCTGCCCCCAATATCTCTCATGAAGGACCCACACTTTTCCACACAGAACTT 1446
Db 2013 CTGAGTGTCTGCCCCCAATATCTCTCATGAAGGACCCACACTTTTCCACACAGAACTT 2072
QY 1447 CTCAGGCTACGACAGCATGTCTGAGTGAAGAAACGCTTCAAGGCTGCCATGATAGTGT 1506
Db 2073 CTCAGGCTACGACAGCATGTCTGAGTGAAGAAACGCTTCAAGGCTGCCATGATAGTGT 2132
QY 1507 TCACCCCTTGTAGTCCACCGGGGGAATAGAGACTCTGAAGCTTCTTCTCTCCCTTCCA 1566
Db 2133 TCACCCCTTGTAGTCCACCGGGGGAATAGAGACTCTGAAGCTTCTTCTCTCCCTTCCA 2192
QY 1567 GTGACAAATGCTGTGTGACACTCTCAAAATGTGTGGGAGAGGCTGTGTGAGGTAGTGTCT 1626
Db 2193 GTGACAAATGCTGTGTGACACTCTCAAAATGTGTGGGAGAGGCTGTGTGAGGTAGTGTCT 2252
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QY 1627 ATGTACAAACTTGTCTTTAAAACTGGAGTTTGCAAGTCAACCTGAGCATACACGCTGAG 1686
Db 2253 ATGTACAAACTTGTCTTTAAAACTGGAGTTTGCAAGTCAACCTGAGCATACACGCTGAG 2312
QY 1687 GCTAGTCAATTTGGCTGATTTATGAACACACAGTTTACAGACAATAATGAGTGGGACCT 1746
Db 2313 GCTAGTCAATTTGGCTGATTTATGAACACACAGTTTACAGACAATAATGAGTGGGACCT 2372
QY 1747 ACATTTGGGATATACCCAAAGCTGGGTAATGATTATCACTGAGAACCCAGCACTCTGGCC 1806
Db 2373 ACATTTGGGATATACCCAAAGCTGGGTAATGATTATCACTGAGAACCCAGCACTCTGGCC 2432
QY 1807 ATGAAGTAATACGGCACTTCCCTGTCAGGCTGTCTGTAGGTTGGTCTGTCTTGCACTG 1866
Db 2433 ATGAAGTAATACGGCACTTCCCTGTCAGGCTGTCTGTAGGTTGGTCTGTCTTGCACTG 2492
QY 1867 CCATGCTCTATGCTGACGACGCTTTTGTAAACATTTTAACTGTTAAATGAATAATC 1926
Db 2493 CCATGCTCTATGCTGACGACGCTTTTGTAAACATTTTAACTGTTAAATGAATAATC 2552
QY 1927 CGTTTGGGAGCTTCTCAAAAAAATAAAAAA 1963
Db 2553 CGTTTGGGAGCTTCTCAAAAAAATAAAAAA 2589

RESULT 3
US-09-886-404-17
; Sequence 17, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung O.
; APPLICANT: Jing, Shujian
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1555)
US-09-886-404-17
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Query Match 50.3%; Score 988.2; DB 10; Length 1841;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;
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QY 6 CAGTGGCGGGCCATGTTGCTAGTGTGCTGATCTTTGGCTGTCATCGTCGAGGAGCGCCCT 65
Db 37 CAGTGGCGGGCCATGTTGCTAGTGTGCTGATCTTTGGCTGTCATCGTCGAGGAGCGCCCT 96
QY 66 GCCTCGAGAGCGCACTATTCACTGTGGCTCTTGAGACAGGGCCATCTCCAGAGTGAATGT 125
Db 97 ACCCGGAGAGCGCACTTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGAATGT 156
QY 126 CCAACACACACTCACTCCAGGAGACTTGAGGACCTCCAGTGGAACTCGTCAAGACAG 185
Db 157 ACAACATGATCTAATCCCGGGAGACTTGAGGAGACTTCGAGTAGAAGCTGTATTCAACATAG 216
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Qy	186	TGTGGCAGCAGAGAGT	TTTCAAATTTTGATGAACATAAAGCTGATCTACCTCCGGCAGACGC	243
Db	217	TGTTGCAACAGGGGAC	TATTTCAATTTTGTATGAATGTAAAGCTGGTACTCCGGCAGATGC	276
Qy	246	CAGCATCGCTGTGTGAAGGCC	ACCAGATCTCGGTGAGTGGCMAAACAACATGAATTC	305
Db	277	CAGCATCGCTGTGTGAAGGCC	ACCAGAATTTGTGTGACGGGCAAAAGCACTTCCAGTC	336
Qy	306	ATACAGCTGTGTGAGGTGCAACT	TACACAGAGGCTTTCCAAAGCCAGACACGACACCTTCCGG	365
Db	337	CTACAGCTGTGTGAGGTGCAAT	TACACAGAGGCTTCCAGACTCAGACACGACACCTCTGG	396
Qy	366	CGGCAATGACATTCCTCTAT	GTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCAT	425
Db	397	TGGTAAATGACATTTTCC	TACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAT	456
Qy	426	CAGCGCCCATAAACAT	CCCCAATCTTAATGAATGAGGACAGCCCTTCTTTGTCTGTGA	485
Db	457	TGGGGCCCATAAAT	TTCTTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGA	516
Qy	486	CTTCACCTCCGCAAGGTG	CCCTAAACCAACGTAATGAATATAAAAGCAGTGCACGTGAGGC	545
Db	517	TTTCACCTCACCAGGTG	CCCTAGACACATATGAATATAAAAGTGTGTCAAGGC	576
Qy	546	GGGAAGCTGTGGGACCC	GACATCACTGCTGTAAAAAGACGAGAAGTGGTTGAAGT	605
Db	577	CGGAAGCTGTGGGAT	CCGAAACATCACTGCTGTGAAGAGATGAGGACAGTAGAAGT	636
Qy	606	GAATTTCAACCAAT	CCCCCTTGGAAACAGATACAGCATTTCTATTCAAACGGGACACGAC	665
Db	637	GAATTTCAACCACT	CCCCCTGGGAACAGATACATGGCTCTTATCCAAACAGCACATAT	696
Qy	666	ATTGGGGTTTTCTAGATG	TCGG-----AGATTAACATGATGAGGAGCTGTGTAGC	716
Db	697	CATCGGGTTTTCTCAG	GTGTTGAGCCACACAGAGAAACAAACGCGAGCTTCAGTGGT	756
Qy	717	CATCCCGGTGACTCAG	GAGAGTGAAGGTGCGGTGTTCAGCTGACCCCATATTTACATAC	776
Db	757	GATTCAGTGACTGGG	GATAGTGAAGGTGCTACGGTGACGCTGACTCCATATTTTCTCTAC	816
Qy	777	CTGGGCAATGACTGC	ATCGACCGCAAGGACAGTTGTGTCTTCTCAGACAGCAAGTGC	836
Db	817	TTGTGGCAGCGACTG	CATCCGACATTAAGGAAACAGTTGTGTCTCTGCCACAAACAGGCGT	876
Qy	837	TCCATCCCTCCAGATG	ACAACAGACGATGCTGGGAGGCTGGCGCTCTCTCTCTCTGGT	896
Db	877	CCCTTTCCCTCTCG	ATAACAAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTCTGCT	936
Qy	897	G---CTGCTGGTGG	CTGTGTGGGTGCTGGCAGCTGGGATCTACCTAACTTGAGGACGAAG	953
Db	937	GTCTCTGCTGGTGC	CACATGGGTGTGTGTGGCAGGGATCTATCTAATGTGGAGGCACGA	996
Qy	954	AAGGACGACGAGACGT	CTCTTTCTATTTCCACCATGCTCTGGCCCTCATTTAAGGTCCT	1013
Db	997	AAGGATCAAGAAGACT	CTCTTTTCTA---CCACCACACTACTGTGCCCCCAATAAGGTTCT	1053
Qy	1014	GGTGGTTATCC	TTCTTGAGATATGTTTCCATCACACCGCTGTGTGCTTCACTGTACTTCT	1073
Db	1054	TGTGGTTTTACCA	CTGTGAATATGTTTCCATCACACAATTTGTGTACTTCACTGTAATTTCT	1113
Qy	1074	TCAAAACTACTG	CAGAAGTGAGTCTATCCCTGAAAATATGGCAGAAAAGAAAATCGCCGA	1133
Db	1114	TCAAAACCATTG	CAGAAGTGAGGTCACTCTCGAAAGTGGCAGAAAAGAAAATAGCAGA	1173
Qy	1134	GATGGGCGGTTAC	AGTGGCTGACCTCAGAAAGCAAGCGGCAGATAAAGTGGTCTTCTCT	1193
Db	1174	GATGGGTCCAGT	CGAGTGGCTTGCCACTCAAAGAAAGGCAGCAGACAAAGTCGTCTTCT	1233
Qy	1194	TCTTCCAGTGAG	CGTCCGACCTTTGTGACAGTGCCTGTGGCCACATATGAGGCGAGGC	1253
Db	1234	TCTTTCCAAATG	ACGTCAACAGTGTGTGCAATGGTACCTGTGTGCAAGACGACGAGGCGATCC	1293
Qy	1254	CAGGAGAACTCT	CAGGATCTGTTCCTCTTGCTTTAACTCTTTTGTAGTGAATTTTCA	1313

RESULT 4

US-09-863-818A-1
; Sequence 1, Application US/09863818A
; Publication No. US20030092881A1

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: APPLICANT: Gorman, Daniel M.
: TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
: FILE REFERENCE: DX01170K
: CURRENT APPLICATION NUMBER: US/09/863,818A
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 607206,862
: PRIOR FILING DATE: 2000-05-24
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 1796

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Query Match

		Best Local Similarity Matches 1241; Conservative	77.9%; Freq. NO: 0;	335; Indels	17; Gaps
Qy	16	GCCAGTTGCTAGTGTTCGATCTTGGCTGCATCGTGCAGGAGCGCCCTCGCTCGAGAG	75		
Db	1	GCAGTGCCTCGTGTCTTAAAGCCTTGGCCGCGCTGTGCAGGAGCGCGTACCCCGAGAG	60		
Qy	76	CCGACTATTCAAGTGTGGCTCTGAGACAGGGCCCATCTCCAGAGTGGATGTGTCCTCAACACACA	133		
Db	61	CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAAATGAT	120		
Qy	136	CTCACTCCAGGAGACTTGAAGGACCTCCAGTCCGAATCGTCAAGACAAAGTGTGGCAGCA	198		
Db	121	CTAATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTACACTAGTGTTCNAACA	180		
Qy	196	GAGAGTTTTCAATTTTGTATGAACATAAGCTGGATCTCCGGGAGACGCCAGCATCCGC	255		
Db	181	GGGGACTATTCAATTTTGTATGAATGTAAAGCTGGGTACTCCGGGACAGTGCACGATCCGC	240		
Qy	256	TTGTTGAAGGCCCAACAGATCTCGCTGAGTGGCAAAAAACAATGAATTCATACAGCTGT	315		

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Db 241 TTGTTGAAGGCCACCAAGATTGTTGTGACGGGCAAAAGCAACTTCAGTCTCTACAGCTGT 300
QY 316 GTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCAAGACCTTCCGCGCCCAATGG 375
Db 301 GTGAGGTGCAATTAACACAGAGGCTTCCAGACTCAGACCAAGACCTCTGGTGTAAATGG 360
QY 376 ACATTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCCAT 435
Db 361 ACATTCTCTATATCGGCTTCCCTGTAGAGCTGAACACAGCTTAATTTCAATTTGGGGCCAT 420
QY 436 AACATCCCAATCTAATATGAATGAGGACAGCCCTTCTTTGCTGTGAACCTTCACTCG 495
Db 421 AATATTCCTAATGAATATGAATGAGATGGCCCTTCCATGCTGTGAATTCACCTCA 480
QY 496 CCAGGTGCTTAAACCAAGCTTAATGAATATAAAGACAGTGCACACTCAGCGGGAACCTG 555
Db 481 CCAGGTGCTGCTAGACCACATATGAATATAAAGAGTGTCAAGGCGCGGAAGCTG 540
QY 556 TGGGACCCAGACATCACTGCTTTGTAAGAACGAGAGATGGTTGAAGTGAATTTTACA 615
Db 541 TGGGATCCGAACATCACTGCTTTGTAAGAAAGATGAGGAGACAGTAGAAGTGAATTTACA 600
QY 616 ACCAATCCCTTGGAAACAGATACAGATTCTCATTTCAAGCGGACACGACATTGGGGTTT 675
Db 601 ACCATCCCTTGGAAACAGATACAGTCTTATCCACACAGCACTATCATCGGGTTT 660
QY 676 TCTAGAGTCTCG-----AGATAAATCTGATGAGGACGCTCTGTAGCCATCCCGGTG 726
Db 661 TCTCAGGTGTTTGAGCCACACACAGAAAGAAACAAACGAGCTTCAGTGGTATTCCAGTG 720
QY 727 ACTGAGGAGTGAAGGTGGGTGGTTTACGTGACCCCATATTTATCATACCTCGCGCAAT 786
Db 721 ACTGGGGATGATGAAGGTGCTACGCTGCAGCTGACTCCATATTTTCTTACTTGTGGCAGC 780
QY 787 GACTGCATCCGACCGAAGGACAGTTGCTTTGTCTGAGACAAAGTGTCTCCATCCCT 846
Db 781 GACTGCATCCGACATGAAGAACAGTTGCTCTGCCCCAACACAGCGTCCCTTTCCCT 840
QY 847 CCAGATGACAAACAGACGATGCTGGAGGCTGGCTGCCTCTCTTCTCTGGT---CTGCTG 903
Db 841 CTGGATAACAAACAAAGCAAGCGGAGGCTGGCTGCCTCTCTCTCTCTGCTGCTG 900
QY 904 GTGGCTGTGGGTGCTGGCAGCTGGGATCTACTTAATCTTGGAGGCAAGGAGGACAG 963
Db 901 GTGGCCACATGGTGTCTGGTGGCAGGATCTATCTAATGTGGAGGCAAGGAGGATCAAG 960
QY 964 AAGAGCTCTTCTTCTATTTCCACATGCTCTGCCCCCTCATTAAGCTCTGTGGTGTAT 1023
Db 961 AAGACTCTCTTTCTA---CCACCACTACTGCCCCCAATTAAGTCTTGTGGTGTAC 1017
QY 1024 CCTTCTGAGATATGTTTCCATCACACCGCTCTGTGCTTCACTGACTTTCTTCAAAACTAC 1083
Db 1018 CCATCTGAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTCAAAACCAT 1077
QY 1084 TGCAGAAGTGAGTGTATCTTGAATAATGGCAGAAAAAGAAATCCCGAGATGGGGCG 1143
Db 1078 TGCAGAAGTGAGTGTATCTTGAATAATGGCAGAAAAAGAAATAGCAGATGGGTCCA 1137
QY 1144 GTACAGTGTGCTGACCACTCAGAGGCAAGCGGAGATGAAGTGTCTTCTTCTTCCAGT 1203
Db 1138 GTGCAAGTGTGCTGCTCACTCAAAAGAGGAGGAGCAGACAAAGTGTCTTCTTCTTCCAAT 1197
QY 1204 GACGTCCCGACCCCTTTGTGACAGTGCCTGTGGCCACAAATGAGGGCAGCGCAGGAGAAC 1263
Db 1198 GACGTCAACAGTGTGCGATGTTACTGTGCAAGAGCGAGGGCAGTCCAGTGAGAAC 1257
QY 1264 TCTCAGGATCTGTTCCTCTTGGCTTTAACTCTTTTGTAGTGAATTTACAGAGCCAGAG 1323
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Db 1318 CATCTGCACAAATACGTGGTGTCTACTTTTAGAGATTTGATACAAAGACGATTAACAT 1377
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QY 1384 GGCCTGAGTGTCTGCCCCCAATATCATATCATGAAGGACGCCACAGCTTTCCACACAGAA 1443
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QY 1444 CTTCTCAAGGCTACGACAGAGCATGTCAAGTGAAGAACGCTCACAAGCCTGCCATGATAGC 1503
Db 1438 CTTCTCCATGTCAAGCAGCAGGTGTCAAGAGGAAAGATCACAAGCCTGCCACGATGGC 1497
QY 1504 TGTTCACCCCTTGTAGTCCACCCCGGGGAA--TAGAGACTCTCTGAAGCCTTCTCTACTCTCC 1561
Db 1498 TGCTGCTCTCTGTAGCCCAACCCATGAGAAGCAAGAGACCTTAAGGCTTCTCTATCCACC 1557
QY 1562 TTCCAGTGAACAATGCTGTGTGACGACTCTGAA 1594
Db 1558 AATTACAGGAAAAAACAAGTGTGATGATCCTGAA 1590
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RESULT 5

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US-09-778-971-1
; Sequence 1, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA of human Evi27
US-09-778-971-1
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Query Match 50.0%; Score 980.8; DB 10; Length 1827;
Best Local Similarity 77.8%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 337; Indels 17; Gaps 4;
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QY 15 GGCCCATGTTGCTAGTGTGCTGATCTTGCTGCATCTGTCAGGAGCGCCCTGCCTCGAGA 74
Db 2 GGGATGTCGCTCGTGTGATGAAGCTGCGCGGCTGTGAGAGGCGCGTACCCGAGA 61
QY 75 GCCGATATTCAAGTGTGCTCTGAGACAGGGCCATCTCCAGAGTGGATGGTCCAAACAC 134
Db 62 GCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAAATGA 121
QY 135 ACTCACTCCAGAGACTTGAGGAGCTCCAGTGGACTCTCCAGTGGACTCTCCAGAGAGTGGCAGC 194
Db 122 TCTAATCCCGGAGACTTGAGGAGCTCCGAGTAGAAGCTGTACAACTAGTGTGTGCAAC 181
QY 195 AGAGGAGTGTTCATATTTGATGAACATAAGCTGGATACTCCGGGAGAGCGCCAGCATCCG 254
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Db 242 CTTGTTGAAGCCACCAAGATTTGTGTACGGGCAAAAAGCAACTTCCAGTCTCTACAGCTG 301
QY 315 TGTGAGTGCACACTACACAGAGGCTTCCAAAGCCAGACACCTTCCGGCGGCAATG 374
Db 302 TGTGAGTGCACATTAACACAGAGGCTTCCAGACTCAGACAGACCTCTGTTGGTAAATG 361
QY 375 GACATTTCTCTATGTAGGCTTCCCTGTGAGCTGAGCACTCTCTATCTCATCAGCGCCCA 434
Db 362 GACATTTCTCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAITGGGGCCCA 421
QY 435 TAACTCCCAATGCTTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGAACCTTCACCTC 494
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Db 422 TAATATTCCTTAATGCAAAATATGAATGAAGATGCGCCCTTCATGCTGTGTGAATTTACCTC 481
Qy 495 GCAGGCTGCTAAACACGCTATGAATATAAAGACGACGCTGAGCGCGGAGCCT 554
Db 482 ACCAGGCTGCTTAGACACATATGAATATAAAGAAAGAGTGTGTCAGGCGGAGCCT 541
Qy 555 GTGGGACCCAGACATCACTCTTTGTAAGAAAGACGAGAGATGTTGAAAGTGAATTTAC 614
Db 542 GTGGGATCCGACATCACTGCTTTGAAGAAAGATGAGGACAGTAGAAGTGAATTTAC 601
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Db 602 AACCACTCCCTTGGGAAACAGATACATGCTCTTTATCCCAACAGCAGCTATCATCGGGT 661
Qy 675 TTCTAGAGTCTGG-----AGATAACTGATGAGGACGCTCTGTAGCCATCCCGT 725
Db 662 TTCTAGGTTGTTGAGCCACACAGAAAGAAACAAACGCGAGCTTCAGTGGTGAATTCAGT 721
Qy 726 GACTGAGGAGAGTGAAGGTGCGGTGCTTCAGCTGACCCATATTTACATACCTCGCGCAA 785
Db 722 GACTGGGATAGTGAAGGTGCTACGCTGAGCTGACTCCATATTTCTTCTACTTGTGGCAG 781
Qy 786 TGACTGCATCCGACGCGAAGGAGCAGTTGTGCTTCTCAGACAAAGTGTCCCATCCC 845
Db 782 CGACTGCATCCGACATAAAGAAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCC 841
Qy 846 TCCAGATGACACAGACGATGCTGGAGGCTGGCTGCTCTCTCTCTGCTG-----CTGCT 902
Db 842 TCTGGATACAAACAAAGAAAGCGGAGGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCT 901
Qy 903 GTGGGCTGTGTGGTGTCTGCGAGCTGGGATCTACCTAACTTGAGGCAAGGAGGAC 962
Db 902 GTGGGCAACATGGTGTGGTGGCAGGATCTATCTAATGTGGAGCAGCAAGAGATCAA 961
Qy 963 GAAGAGCTCTTTCTTATTTCCACCATGCTCTGCTCCCTCATTAAGGTCTCTGCTGTTTA 1022
Db 962 GAAGAGCTCTTTCTTCTA---CCACACACTACTGCTCCCTCATTAAGGTCTCTGCTGTTTA 1018
Qy 1023 TCTTCTGAGATATGTTTCCATCAGACCGCTGTGCTGCTTCACTGACTTCTTCAAACTA 1082
Db 1019 CCATCTGAATATGTTTCCATCAGACAAATTTGTTACTTCACTGAATTTCTTCAAACTA 1078
Qy 1083 CTGCAAGTGTAGGTCTATCTTTGAAATATGGCAGAAAGAAATCGCGAGATGGGCG 1142
Db 1079 TTGCAAGTGTAGGTCTATCTTTGAAATATGGCAGAAAGAAATAGCAGATGGGTCC 1138
Qy 1143 GTTACAGTGGCTGACCATCAGAACGAGCGGAGATAAGTGTCTCTTCTTCTCCAG 1202
Db 1139 AGTGCAAGTGGCTTGCCACTCAAAGAAAGCAGCAGACAAAGTCTTCTTCTTCCAA 1198
Qy 1203 TGACGTCCCGACCTTTGTGACAGTGCCTGTGGCCACATGAGGCGAGCGCCAGGAGNA 1262
Db 1199 TGACGTCAACAGTGTGTGGATGGTATCTGTCACGATGAGGCGAGCGGCGAGTGA 1258
Qy 1263 CTCTCAGGATCTGTTCCCTCTTGCCTTTAACTCTTTTGTAGTGAATTCAGCAGCAGAC 1322
Db 1259 CTCTCAGACCTCTTCCCTCTTGCCTTTAACTCTTCTGATGATCTAAGAGCGCAGT 1318
Qy 1323 GCATCTGCAAAATACCTGGTGTATCTTGGGGAGCAGACCTCAAAGGCGACTATAA 1382
Db 1319 TCATCTGCAAAATACCTGGTGTCTCTTTAGAGAGATTTGATACAAAGAGCGATTACAA 1378
Qy 1383 TGCCCTGAGTGTCTGCCCCATATCATCTCATGAGGAGCGCAGCTTTCCACACAGA 1442
Db 1379 TGCTCTCAGTGTCTGCCCCAAGTACATCTTCATGAAGGATGCCACTGCTTTCTGTGCGA 1438
Qy 1443 ACTTCTCAAGGCTACGACAGCATGTGCTGAGGAAGAAAGCTCACAAGCTGCGCATGATAG 1502
Db 1439 ACTTCTCAGTGTCAAGCAGCAGGTGTGACGAGGAAAGATCACAAGCTGCGCATGATG 1498
Qy 1503 CTGTTACCTCTGTAGTCCACCGGGGAA--TAGAGACTCTGAAGCCTTCTACTCTCC 1560

Db 1499 CTGCTGCTCTTGTAGCCACCCATGAGAAGCAAGACGCTTAAAGGCTTCTATCCAC 1558
Qy 1561 CTTCCAGTGACAAATGCTGTGTGACGACTCTGAA 1594
Db 1559 CAATTACAGGAAAAAACGTTGTGATGATCCTGAA 1592

RESULT 6

US-09-874-503-11
; Sequence 11, Application US/09874503
; Patent No. US20020177188A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah G.
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa A.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: 11-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P3 (US)
; CURRENT APPLICATION NUMBER: US/09/874,503
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/138,387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: US 60/134,287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: US 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-20
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 09/380,138

; PRIOR FILING DATE: 1999-08-25
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US PCT/US00/34956
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: US PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US PCT/US00/30873
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR APPLICATION NUMBER: US PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: US PCT/US00/07532
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US PCT/US00/05841
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US PCT/US00/05601
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: US PCT/US00/04341
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: US PCT/US99/31274
 ; PRIOR FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: US PCT/US99/10733
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US PCT/US99/05028
 ; PRIOR FILING DATE: 1999-03-08
 ; NUMBER OF SEQ ID NOS: 39
 ; SEQ ID NO 11
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-874-503-11

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
 Best Local Similarity 78.7%; Pred. No. 3e-313;
 Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

QY 13 CGGGCCATCTGCTAGTGTGCTGATCTTGGCTGATGTCGAGGAGCGCCCTGCTCGA 72
 DB 1 CGGGCGATGTGCTGCTGTCTGATGCTTAAAGCTGGCGCGCTGTGAGGAGCGCGTACCCCGA 60
 QY 73 GAGCCGACTATTCAAGTGTGGCTCTGAGACAGGGCCATCTCCAGTGGATGGTCCAAACAC 132
 DB 61 GAGCCGACGTTCAATGTGGCTCTGAACTGGCCATCTCCAGTGGATGCTAGAACAT 120
 QY 133 ACATCACTCCAGGAGACTTGGAGGACCTCCAAAGTGGAACTGTCAGAACAAAGTGTGGCA 192
 DB 121 GATCTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCA 180
 QY 193 GCAGAGGAGTTTCAATTTTGTATGACATAGCTGATGATCTCGGGCAGACGCCAGCATC 252
 DB 181 ACAGGGGAGCTATTCAATTTTGTATGAACTGAACTGGGTACTCCGGCAGATGCCAGCATC 240
 QY 253 CGCTTCTTGAAGGCCACCAAGATCTCGGTGAGTGGCAAAACAAATGAAATTCATACAGC 312
 DB 241 CGCTTGTGAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCAGCTCTACAGC 300
 QY 313 TGTGTGAGGTGCAACTACACAGAGGCTTTCCAAAGCCAGACAGACCTTCCCGCGGCAAA 372
 DB 301 TGTGTGAGGTGCAATTTACACAGAGGCTTTCCAGACTCAGACACAGACCTTCTGTGTGATA 360
 QY 373 TGGACATTTCTCTATGAGGCTTCCCTGTGGAGCTGAGCATCTCTATCTCATCAGCGGC 432
 DB 361 TGGACATTTCTCTATGAGGCTTCCCTGTGTGAGCTGAGCATCTCTATCTCATCAGCGGC 420
 QY 433 CATACATCCCAATGCTAATATGATGAGGACAGCCCTTCTTTGCTGTGAACTTCACC 492
 DB 421 CATATATTTCTTAATGCAATATGATGAGGATGGCCCTTCCATGCTGTGAAATTTACC 480
 QY 493 TCGCCAGGCTGCTTAAACCACGTAATGAAATATAAAAGCAGTGCACTGAGGCGGGAAGC 552

DB 481 TCACCAGGCTGCTAGACCACATAATGAAATATAAAAAAAGTGTCTCAAGGCCGGAAGC 540
 QY 553 CTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACAGAGATGTTTGAAGTGAATTTTC 612
 DB 541 CTGTGGGATCCGAACATCACTGCTTGTAAAGAAATGAGAGACAGTAGAAGTGAATTTTC 600
 QY 613 ACAACCAATCCCTTTGGAAACAGATACACGATTTCTCAATTCACGGGACACGACATTTGGGG 672
 DB 601 ACAACCACTCCCTGGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGG 660
 QY 673 TTTTCTAGAGTCTGG-----AGATAAATGATGAGGACGCTCTGTAGCCATCCCG 723
 DB 661 TTTTCTCAGGTGTTTGAAGCCACACCCAGAAAGAAACAAACCGAGCTTTCAGTGGTATTTCA 720
 QY 724 GTGACTGAGGAGAGTGAAGGTGGTGTTCAGCTGACGCCCATATTTATACATACCTCGCGG 783
 DB 721 GTGACTGGGATGAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC 780
 QY 784 AATGACTGCATCCGACGCGAAGGACAGTTGTGCTTTGTCTAGAGACAAAGTGTCTCCATC 843
 DB 781 AGCGACTGCATCCGACATAAAGGAAACAGTTGTGCTCTGCCCAAAACAGCGCTCCCTTTTC 840
 QY 844 CCTCCAGATGACAAACAGACGCTGCTGGAGGCTGGCTGCTCTCTTCTGTGTG---CTG 900
 DB 841 CCTCTGGATAACAAACAAAGCAAGCGGAGGCTGGCTGCTCTCTCTCTGTGTCTGTG 900
 QY 901 CTGGTGGCTGTGTGGTGTGCTGCGAGCTGCTGAGCTGAGTAACTTGGAGGCAAGGAAGGAC 960
 DB 901 CTGGTGGCCACATGGTGTGCTGGTGGAGGATCTATCTAATGTGGAGGCAAGGAAGATC 960
 QY 961 AGCAAGACGCTCTCTTCTTCCATTTTCCACCATGCTCTGCCCCCTCATTAAGGTCTCTGGTGT 1020
 DB 961 AAGAAGACTTCTTTCTA---CCACCACACTACTGCCCCCATTAAGGTCTCTGTGGTT 1017
 QY 1021 TATCTTCTGAGATATGTTTCCATCACACGCTGTGCTGCTTCACTGCTTCTTCTTCAAAAC 1080
 DB 1018 TACCCATCTGAAATATGTTTCCATCACACATTTGTTACTTCACTGAAATTTCTTCAAAAC 1077
 QY 1081 TACTCAGAAAGTGAAGTCACTCTTGAATAATGCGAGAAAAGAAATCCCGAGATGGGG 1140
 DB 1078 CATTCAGAAAGTGAAGTCACTCTTGAATAATGCGAGAAAAGAAATACAGAGATGGGT 1137
 QY 1141 CGGTGACAGTGGCTGACCACTCAGAAAGCAAGCGGAGATAAAGTGGTCTTCTTCTTCCC 1200
 DB 1138 CCAGTGCAGTGGCTTGGCACTCAAAGAGGAGCAGACAGCAAAAGTCTCTTCTTCTTCC 1197
 QY 1201 AGTACGCTCCGACCCCTTGTGACAGTGTGCTGTGGCAAAATGAGGCGAGCGCCAGGAG 1260
 DB 1198 AATGACGTCAACAGTGTGTGCGATGTACTCTGGCAAGAGCGAGGCGAGTCCAGTGAG 1257
 QY 1261 AACTCTCAGGATCTGTCCTCTTCCCTTAACTCTTTTGTAGTATTTTCAAGGCCAG 1320
 DB 1258 AACTCTCAAGACCTCTTCCCTTAACTCTTTCAGTGTATCTAAGAGGCCAG 1317
 QY 1321 AGCATCTGCAAAATACCTGGTGGTCTATCTTGGGAGAGCAGACCTCAAAGCGCACTAT 1380
 DB 1318 ATTCTCTGCAAAATACGTTGGTGGTCTACTTTAGAGAGATTGATACAAAAGCGATTAC 1377
 QY 1381 AATGCCCTGAGTGTCTGCCCCCAATATCATCTCAAGAGGACGCCACAGCTTTTCCACACA 1440
 DB 1378 AATGCTCTCAGTGTCTGCCCCCAAGTACCACTCATGAAGGATGCCACTGCTTCTGTGCA 1437
 QY 1441 GAATCTTCAAGGCTACCGAGAGCATGTGAGTGAAGAACGCTCACAGGCTTGCCTGAT 1500
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 QY 1501 AGCTGTTCACCTCTGTAG 1518
 DB 1498 GGCTGCTGCTCTTGTAG 1515

	PRIOR FILING DATE: 2001-07-30	
	PRIOR APPLICATION NUMBER: 09/929404	
	PRIOR FILING DATE: 2001-08-13	
	PRIOR APPLICATION NUMBER: 09/931836	
	PRIOR FILING DATE: 2001-08-16	
	PRIOR APPLICATION NUMBER: PCT/US99/05028	
	PRIOR FILING DATE: 1999-03-08	
	PRIOR APPLICATION NUMBER: PCT/US99/10733	
	PRIOR FILING DATE: 1999-05-14	
	PRIOR APPLICATION NUMBER: PCT/US99/31274	
	PRIOR FILING DATE: 1999-12-30	
	PRIOR APPLICATION NUMBER: PCT/US00/04341	
	PRIOR FILING DATE: 2000-02-18	
	PRIOR APPLICATION NUMBER: PCT/US00/05601	
	PRIOR FILING DATE: 2001-03-01	
	PRIOR APPLICATION NUMBER: PCT/US00/05841	
	PRIOR FILING DATE: 2000-03-02	
	PRIOR APPLICATION NUMBER: PCT/US00/07532	
	PRIOR FILING DATE: 2000-03-21	
	PRIOR APPLICATION NUMBER: PCT/US00/15264	
	PRIOR FILING DATE: 2000-06-02	
	PRIOR APPLICATION NUMBER: PCT/US00/23328	
	PRIOR FILING DATE: 2000-08-24	
	PRIOR APPLICATION NUMBER: PCT/US00/30873	
	PRIOR FILING DATE: 2000-11-10	
	PRIOR APPLICATION NUMBER: PCT/US00/32678	
	PRIOR FILING DATE: 2000-12-01	
	PRIOR APPLICATION NUMBER: PCT/US00/34956	
	PRIOR FILING DATE: 2000-12-20	
	PRIOR APPLICATION NUMBER: PCT/US01/06520	
	PRIOR FILING DATE: 2001-02-28	
	PRIOR APPLICATION NUMBER: PCT/US01/17800	
	PRIOR FILING DATE: 2001-06-01	
	PRIOR APPLICATION NUMBER: PCT/US01/19692	
	PRIOR FILING DATE: 2001-06-20	
	PRIOR APPLICATION NUMBER: PCT/US01/21066	
	PRIOR FILING DATE: 2001-06-29	
	PRIOR APPLICATION NUMBER: PCT/US01/21735	
	PRIOR FILING DATE: 2001-07-09	
	NUMBER OF SEQ ID NOS: 39	
	SEQ ID NO 11	
	LENGTH: 1515	
	TYPE: DNA	
	ORGANISM: Homo Sapien	
	US-10-000-157-11	
	Query Match 49.1%; Score 963.6; DB 9; Length 1515;	
	Best Local Similarity 78.7%; Pred. No. 3e-313;	
	Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps	
Qy	13 CGGGCCACTGTTGTAGTGTTCATCTCGCTGCATCGTGACAGGAGCGCCCTGCCCTCGA 72	
Db	1 CGGGCGATGTCGCTCGCTGCTGAAGCTCGGCCGCTGTGACAGGAGCGCCGTACC	
Qy	73 GAGCCGCACTATTTCAGTGTGCTCTGACAGAGGGCCCATCTCCAGATGGATGGTCCAACAC 132	
Db	61 GAGCCGACCGCTTCAAATGTCCTCTGAACCTGGGCCCATCTCCAGATGGATGGTCCAACAT 120	
Qy	133 ACACCTACTCCAGAGACTTTGAGGGACCTCCAAAGTGGAACTCCTCAAGACAAGTGTGGCA 192	
Db	121 GATCTAATCCCGGAGACTTTGAGGGACCTCCGAGTAGAACCTGTTACAACCTAGTGTGCA 180	
Qy	193 GCAGAGAGTTTTTCAATTTTGTATGAACATAAGCTGGATACTCCGGGCAGACGCCAGATC 252	
Db	181 ACAGGGGACTATTTTCAATTTTGTATGAATGTAAAGCTGGGTACTCCGGGCAGATGCCAGATC 240	
Qy	253 CGCTTGTGTGAAGGCCACCAAGATCTCGCTGAGTGGCAAAAACAAACATGAATTCATACAGC 312	
Db	241 CGCTTGTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCNAGTCTTACAGC 300	
Qy	313 TGTGTGAGGTGCAACTACACAGAGGCGCTTCCAAAGCCAGACCAAGACTTCCCGCGCGCAA 372	
Db	301 TGTGTGAGGTGCAATTACACAGAGGCGCTTCCAGACTCACACACAGACCTCTCGTGTGTAA 360	

QY 373 TGAACATTTCTCTATGTAGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
Db 361 TGAACATTTCTCTATGTAGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 420
QY 433 CATAACATCCCAATGCTAATATGATGAGGACAGCCCTCTTTGCTGTGAATTCACC 492
Db 421 CATAATATTTCTAATGCAATATGATGAGGACAGCCCTCTTTGCTGTGAATTCACC 480
QY 493 TGGCAGGCTGCTTAACCAACAGCTAATGAATATAAAGAGCAGTGCACTGAGCGGGAAGC 552
Db 481 TCACCAAGGCTGCTAGACACATATGAATATAAAGAGGCTGCTCAAGCGCGAAGC 540
QY 553 CTGTGGGACCCAGACATCACTGCTTTGAAAGAAAGAGAGATGTTGAAAGTGAATTC 612
Db 541 CTGTGGGATCCGAACATCACTGCTTTGAAAGAAAGAGAGATGTTGAAAGTGAATTC 600
QY 613 ACACCAATCCCTTGGAAACAGATACAGATCTCTATTCAACGGGACAGCATTTGGGG 672
Db 601 ACACCACTCCCTTGGAAACAGATACAGATCTCTATTCAACAGACACTATCATCGGG 660
QY 673 TTTTCTAGAGTGTGG-----AGAATAAACTGATGAGGACGCTCTGTAGCCATCCCG 723
Db 661 TTTTCTCAGTGTGTTGAGCCACACAGAGAAACAAACGCGACTTCAGTGGTATCCA 720
QY 724 GTGACTGAGGAGTGAAGTGGTGGTTCAGCTGACCCCATATTTATCATCTCGGGC 783
Db 721 GTGACTGGGGATGTAAGGTGCTACGGTGCAGCTGACTCCATATTTCTACTTGTGGC 780
QY 784 AATGACTGATCCGACGAGGAGCAGTGTGCTTTGCTCAGACAAAGTGTCCCATC 843
Db 781 AGCAGTGTATCCGACATAAAGAGAAAGTGTGCTGTGCCCAACAAACAGCGCTCCCTTC 840
QY 844 CTCCAGATGACAAACAGACGCTGCGGAGGCTGCTCTCTCTCTGTTG---CTG 900
Db 841 CTCTGATTAACAAACAAAGCAAGCGGAGGCTGCTCTCTCTCTGTTGTTCTCTG 900
QY 901 CTGTGGTGTGTGGTGTGCTGGAGCTGGGATCTACCTAACTTGGAGGCAAGGAAGAC 960
Db 901 CTGGTGGCACATGGTGTGCTGGGAGGATCTATCTAATGTGGAGGACAGAAAGGATC 960
QY 961 ACAGACGCTCTCTCTATTTCCACATGCTCTGCTGCTCTCTCTCTCTCTGTTGTT 1020
Db 961 AAGAAGCTCTCTCTCTCTA---CCACCACTACTCTCTCTCTCTCTCTCTCTCTGTT 1017
QY 1021 TATCTCTGAGATATGTTTCCATCACCGCTGCTGCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1018 TACCACTCTGAATATGTTTCCATCACCAATTTGTTACTTCTCACTGATTTCTTCAAAC 1077
QY 1081 TACTGAGAAGTGAAGTCTATCTCTTGAATAATGGCAGAAAAAGAAATCGCCGAGATGGG 1140
Db 1078 CATTCGAGAAGTGAAGTCTATCTCTTGAATAATGGCAGAAAAAGAAATAGCAGAGATGGT 1137
QY 1141 CCGGTACGTGGTGAACCTGAGAGCAAGCGGAGATTAAGTGTCTCTCTCTCTCTCTCC 1200
Db 1138 CCAAGTGAAGTGGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
QY 1201 AGTGAGTCTCCGACCTCTTGTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1198 AATGAGCTCAACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1257
QY 1261 AACTCTCAGGATCTGTCT 1320
Db 1258 AACTCTCAGGATCTGTCT 1317
QY 1321 AGCATCTGCAACAAATACCTGTGTGTCTATCTTGGGGGAGCAGACCTCAAGGCGACTAT 1380
Db 1318 ATTCTCTGCAACAAATACGTTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1377
QY 1381 AATGCCCTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 1378 AATGCTCTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1437

QY 1441 GAACCTTCTCAAGGCTACGAGAGCATGTCTAGTGAAGAAAGCTCACAAGCCCTGCCATGAT 1500
Db 1438 GAACCTTCTCTATGTCTCAAGCAGCAGGTGTCTAGCAGGAAAAAGATCAAGCTTCCACGAT 1497
QY 1501 AGCTGTTCACCCCTTTGTAG 1518
Db 1498 GGCTGCTGCTCTTTGTAG 1515
RESULT 8
US-10-063-547-157
; Sequence 157, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-157

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
QY 13 CGGGCCATGTTCTCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 72
Db 1 CGGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 73 GAGCGGACTATTCAGTGTGGCTCTGAGACAGGCGCCATCTCCAGAGTGGATGCTCCAAAC 132
Db 61 GAGCGGCGTTCANTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTCAACAT 120
QY 133 ACATCTACTCCAGGAGACTTGAGGACCTCCAAAGTGGAACTCGTCAAGCAAGTGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTGAGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCA 180
QY 193 GCAGAGGAGTTTTCATTTTGTGATGACATAGCTGGATCTCCGGGACAGCCGAGCATC 252
Db 181 ACAGGGGACTATTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 253 CGCTTGTGTAAGGCCCAACAAAGATCTCGGTGAGTGGCAAAACAAATGAATTCATACAGC 312
Db 241 CGCTTGTGTAAGGCCCAACAAAGATTTGTGTGACGGGCAAAAGCACTTCAGTCTACAGC 300
QY 313 TGTGTAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGCGGCAAA 372
Db 301 TGTGTAGGTGCAATTAACACAGAGGCTTCCAGACTCCAGACAGACCCCTCTGTTGGTAA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
Db 361 TGGACATTTCTCTATGTAGGCTTCCCTGTTGGAGCTGAGCACTCTATTTCTATTTGGGGCC 420
QY 433 CATAACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGCTGTGAATTCACC 492
Db 421 CATAATATTTCTAATGCAATATGAATGAGATGGCCCTTCCATGTCTGTGAATTCACC 480
QY 493 TCGCCAGGCTGCTTAACCAACCACTAATGAATAATAAAGAGCAGTGCCTGAGCGGGAGC 552

Db 61 GAGCCGACGTTCAATGTGGCTCTGAACCTGGGCCATCTCCAGAGTGGATGCTACAACAT 120
QY 133 ACACCTCACTCCAGGAGACTTGAGGACCTCAAAGTGAACTCGTCAAGACAAGTGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTGAGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCA 180
QY 193 GCAGAGAGTTTCAATTTTGTAGAACATAGCTGGATCTCGGCGAGAGCCGACGATC 252
Db 181 ACAGGGGACTATTCAATTTTGTAGTAATGTAAGCTGGGTACTCCGGCGAGATGCCGACATC 240
QY 253 CGCTTGTGAAGGCCACCAAGACTCGGTGAGTGCGGCAAAACAAATGAAATTCATACAGC 312
Db 241 CGCTTGTGAAGGCCACCAAGATTGTGTGACGGGCAAAAGCAACTTCAGTCTCTACAGC 300
QY 313 TGTGTGAGGTGCAATACACAGAGGCTTCCAAAGCCGAGACCAAGACTTCCCGCGGCAAA 372
Db 301 TGTGTGAGGTGCAATACACAGAGGCTTCCAGACTCAGACCAAGACCTCTCGTGTGTA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTATCTCATCAGGGCC 432
Db 361 TGGACATTTTCTTACATCGGCTTCCCTGTAGAGCTGAACACACAGTCTATTTCATTGGGGCC 420
QY 433 CATACATCCCAATGCTAATGATGAGGACAGCCCTTCTTGTGCTGTGAATTCACC 492
Db 421 CATATATTCTTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTCACC 480
QY 493 TCGCCAGGCTGCTTAACCAACGAGTAATGAATATAAAAGCAGTGCACTGAGCGGGAAGC 552
Db 481 TCACCAAGGCTGCTAGACCAACATAATGAATATAAAAGATGTGTCAAGGCCGGAAGC 540
QY 553 CTGTGGGACCCAGACATCTCTGTGTAAAGAAAGAGAGATGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAACATCACTGTCTGAAGAAGAAATGAGGAGACAGTAGAAGTGAATTC 600
QY 613 ACAACCAATCCCTTGGAAACAGATACAGATTCTCATTCACGGGACACAGATTGGGG 672
Db 601 ACAACCACTCCCTTGGAAACAGATACAGTCTTATCCAAACACAGCACTATCATCGGG 660
QY 673 TTTTCTAGAGTGTGG-----AGAATAAACTGATGAGGACGCTCTGTAGCCATCCCG 723
Db 661 TTTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGAGCTTCAGTGTGATTCGA 720
QY 724 GTGACTGAGAGTGAAGTGGGTGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 783
Db 721 GTGACTGGGGTAGTGAAGTGTCTAGGTCAGCTGAGTCACTCACTATTTCTACTTGTGC 780
QY 784 AATGACTGATCCGACGCGAAGGACAGTGTGCTTTGCTCAGAGACAAGTGTCCCATC 843
Db 781 AGCGACTGATCCGACATAAAGGAACAGTGTGCTGTGCCCAAAACAGCGCGTCCCTTC 840
QY 844 CTTCCAGATGACACAGACGATGCTGGGAGGCTGCTCTCTCTCTGTTG---CTG 900
Db 841 CTTCTGGATAACAAAGAAAGACGCGGAGGCTGCTGCTCTCTCTCTGTTCTG 900
QY 901 CTGGTGGCTGTGTGGTGTGCGAGCTGGGATCTACCTAACTTGGAGGCAAGGAAGAGC 960
Db 901 CTGGTGGCCACATGGTGTGCTGGTGGCAGGATCTATCTAATGTGGAGGACAGAAAGATC 960
QY 961 ACGAAGAGCTCCTTCTTCTATTTCCACCATGCTCTCTGCTCTCTCTCTCTCTCTCTCT 1020
Db 961 AAGAAGACTTCTCTTTCTA---CCACCACTACTGCCCCCTTAAAGTGTCTTGTGGTT 1017
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Db 1018 TACCACTCTGAATATGTTTCTATCACAAATTTGTACTTCACTGAATTTCTTCAAAAC 1077
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QY 1141 CCGGTACAGTGGCTGACCTCAGAGCAAGCGGAGATAAAGTGTCTCTCTCTCTCTCTCC 1200

Db 1138 CCAGTGCAGTGGCTTGCCTCAAAAGAGGAGCAGACAAAGTGTCTTCTCTTTCC 1197
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Db 1198 AATGACGTCACAGTGTGTGCGATGCTGTGGCAAGAGCGAGCGAGTCCAGTGTGAG 1257
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Db 1258 AACTCTCAAGACCTCTTCCCTTTAACCCTTTTGTAGTGTATTTAAGAGCCAG 1317
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Db 1318 ATTATCTGCACAAATACCTGTGTGTCTACTTTAGAGAGATTGATACAAAGACGATTAC 1377
QY 1381 AATGCCCTGAGTGTGTGCCCCCAATATCATCTCATGAAGGACGCGACAGCTTTCCACACA 1440
Db 1378 AATGTCTCAGTGTGTGCCCCAAGTACCACTCATGAAGGATGCCACTGCTTTCTGTGCA 1437
QY 1441 GAACTTCTCAAGGCTACGAGAGCATGTCTGAGTGAAGAAAGCTCACAAGCCTGCCATGAT 1500
Db 1438 GAACTTCTCCATGTCAAGCAGCAGGTGTGAGGAGAAAGATCAAGCCTGCCACGAT 1497
QY 1501 AGCTGTTTCAACCCTTGTAG 1518
Db 1498 GCGTGTGCTCTCTTGTAG 1515

RESULT 10
US-10-174-590-399
; Sequence 399, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-399

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

QY 13 CCGGCGATGTTCTAGT 72
Db 1 CCGGCGATGTTCTGCTGT 60
QY 73 GAGCGGACTTATTCAGT 132
Db 61 GAGCGGACGTTTCAATGT 120
QY 133 ACACCTCACTCCAGGAGACTTGAGGAGCTTCCAAAGTGGAACTCGTCAAGACAAGTGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTGAGGAGCTTCCGAGTAGAACCTGTTACAACTAGTGTGCA 180
QY 193 GCAGAGAGTGTTCATTTTGTATGAACATAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252

Db 301 TGTGTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACGAGCCCTCTGTGTGTAA 360
Qy 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
Db 361 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTATCTCATCAGCGCC 420
Qy 433 CATACATCCCAATGCTTAATGAATGAGGACAGCCCTCTTTGTGTGTGAATCTCAAC 492
Db 421 CATATATTTCTTAATGAATGAGGATGAAGATGGCCCTTCCATGTCTGTGAATTTCAAC 480
Qy 493 TGGCAGGCTGCTTAACACGCTTAATGAATATAAAGAGCTGCACTGAGCGGGAAGC 552
Db 481 TACACAGGCTGCTTACACACATTAATGAATATAAAGAGCTGCACTGAGCGGGAAGC 540
Qy 553 CTGTGGAGCCAGACATCACTGCTTGTAAAGAGGAGAGAGTGTGAAGTGAATTTTC 612
Db 541 CTGTGGAGCCGACATCACTGCTTGTGAAGAGAGGAGACAGTGAAGTGAATTTTC 600
Qy 613 ACACCAATCCCTTGGAAACAGATACAGATTTCTCATTTCAACGGGACAGCAATTTGGG 672
Db 601 ACACCACTCCCTTGGAAACAGATACAGATTTCTCATTTCAACAGCACTATCATCGG 660
Qy 673 TTTTCTAGAGTGTGG-----AGATAAAGTATGAGGAGCTGTAGCCATCCCG 723
Db 661 TTTTCTAGAGTGTGGAGCCACACAGAGAGAAACAAACGAGCTTCAAGTGTATTTCA 720
Qy 724 GTGACTGAGGAGAGTGAAGTGGGTGTTTCACTGACGCCCATATTTACATCTCGGC 783
Db 721 GTGACTGGGGATGAGAGTGTACGGTGCAGCTGACCTCATTTTCTACTTGTGGC 780
Qy 784 AATGACTGCATCCGACGGAAGGAGAGTGTGTTTGTCTCAGAGACAAAGTGTCTCCATC 843
Db 781 AGCGACTGCATCCGACATTAAGAGAAAGTGTGCTCTGCCCAACAAAGCGTCCCTTTC 840
Qy 844 CTTCCAGATGACACAGAGCATGCTGGAGAGCTGCTGCTCTCTCTCTGTTG---CTG 900
Db 841 CTTCTGGATTAACAAACAAAGAGGAGGAGGCTGCTGCTCTCTCTCTGTTGTTG 900
Qy 901 CTGTGGCTGTGTGGTGTCTGGAGCTGGATCTACTTAACCTTGGAGGCAAGAGGAGC 960
Db 901 CTGTGGCCACATGGTGTCTGGGAGGAGGCTGCTGCTCTCTCTCTCTGTTGTTG 960
Qy 961 ACGAAGAGTCTCTTTCTATTTTCCACCATCTCTGCTGCTGCTCTCTCTCTCTCTCT 1020
Db 961 AAGAAGACTCTCTTTCTA---CCACACACTACTGCTGCTGCTGCTGCTGCTGCTGTT 1017
Qy 1021 TATCTCTGAGATATGTTTCCATCACCGCTGTGCTTCACTGACTTTCTTCAAAAC 1080
Db 1018 TACCCATCTGAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTCAAAAC 1077
Qy 1081 TACTGAGAGTGAAGTCTATCTTGAATAATGGCAGAAAAAGAAATCGCGAGATGGGG 1140
Db 1078 CATTCGAGAGTGAAGTCTATCTTGAAGAGTGGCAGAAAAAGAAATAGCAGAGTGGT 1137
Qy 1141 CCGGTACAGTGGCTACCACTCAGAGAGGAGGAGAGTAAAGTGTCTCTCTCTCTCTCT 1200
Db 1138 CCAGTGCAGTGGCTTCCCACTCAAAAGAGGAGGAGCAGACAAAGTGTCTCTCTCTCT 1197
Qy 1201 AGTACGTCGAGCCCTTTGTGACAGTGTCTGTGGCCCAATGAGGGGAGCGCCAGGAG 1260
Db 1198 AATGAGTCAACAGTGTGTGATGTGTACCTGTGGCAGAGGAGGAGGAGTCCAGTGAG 1257
Qy 1261 AACTCTCAGATCTGTCT 1320
Db 1258 AACTCTCAGAGCT 1317
Qy 1321 AGCATCTGCACAAATACCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1318 ATTCACTGCACAAATACCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1377
Qy 1381 AATGCCCTGAGTGTCTGCCCCCAATATCATCTCATGAAGGAGCGCCACAGCTTTCCACA 1440

Db 1378 AATGTCTCAGTGTCTGTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGA 1437
Qy 1441 GAATTTCTCAAGGCTACGACAGAGCATGTGAGTGAAGAAACGCTCAAGAGCTGCGCATGAT 1500
Db 1438 GAATTTCTCAGTGTCAAGCAGCAGGCTGTGAGCAGGAAAGATCACAAGCTGCCAGAT 1497
Qy 1501 AGCTGTTTCACTTGTGTAG 1518
Db 1498 GGCTGTCTCTCTGTGTAG 1515
RESULT 12
US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157
Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
Qy 13 CGGGCCATGTTCTAGTGTGTGATCTTTGGTGTGATCTGTGAGGAGCGCCCTGCTCGA 72
Db 1 CGGGCGATGTCTGTCTGTCTAAGCCCTGGCGGCTGTGAGGAGCGCCCTGATCCCGA 60
Qy 73 GAGCGCATTTTCACTGTGGCTCTGAGCAGCGCCATCTCCAGAGTGGATGTCNAACAC 132
Db 61 GAGCGCATTTTCACTGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGTACAACAT 120
Qy 133 ACACCTCACTCCAGGAGACTTGAAGGAGCCTCCAAAGTGGAACTCTCAAGACAAGTGTGGA 192
Db 121 GATCTAATCCCGGAGACTTGAAGGAGCCTCCAGTAGAACCTGTTACACTAGTGTGA 180
Qy 193 GCAGAGAGTTTTCAATTTTGTATGAACATAAGCTGGATACTCCGGGAGAGCCCGAGCATC 252
Db 181 ACAGGGAGCTATTTCAATTTTGTATGAATGTAAGTGGTACTCCGGGAGATGCCAGCATC 240
Qy 253 CGCTTGTGAAGGCCACCAAGATCTGCGTGTGAGTGGCAAAACAAATGATGATCATACAGC 312
Db 241 CGCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGC 300
Qy 313 TGTGTGAGTGTCAACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGGCGCAAA 372
Db 301 TGTGTGAGTGTCAATTTACAGAGGCTTCCAGACTCAGACAGACCTTCTGTGTGTAA 360
Qy 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
Db 361 TGGACATTTCTCTATCGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAATTTGGGCC 420
Qy 433 CATACATCCCAATGCTTAATGAATGAGGACAGCCCTTTTGTGTGTGAATTTTCAAC 492
Db 421 CATATATTTCTTAATGAATGAATGAATGAGGATGGCCCTTCCATGTCTGTGAATTTTCAAC 480

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QY 493 TCGCCAGGCTGCTAAACCAACGTAATGAAATATAAAAAAGCAGTGCACTGAGCGGGAAGC 552
Db 481 TCACCAAGGCTGCTAGACCACATATGAAATATAAAAAAGTGTCTCAAGCGCGGAAGC 540
QY 553 CTGTGGGACCCAGACATCATCTGCTTTGTAAGAAAGACAGAGATGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAACATCATCTGCTTTGTAAGAAAGATGAGGAGACAGTAGAAGTGAATTC 600
QY 613 ACAACCAATCCCTTGGAAACAGATACAGATTCTCATTTCAACGGGACAGCATTTGGG 672
Db 601 ACAACCACTCCCTTGGAAACAGATACATGCTCTTATCCAAACAGCACTATCATCTCGG 660
QY 673 TTTTCTAGAGTGTGCG-----AGATAAACTGATGAGGACGCTCTGTAGCCATCCCG 723
Db 661 TTTTCTCAGTGTGTTGAGCCACACACAGAGAAACAAACGCGAGCTTCACTGTGATTCCA 720
QY 724 GTGACTGAGGAGTGAAGTGGGTGTTGAGTGAACCCCATATTTATCATACCTGCGGC 783
Db 721 GTGACTGGGGATGTTGAAGTGTCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC 780
QY 784 AATGACTGCATCGGACCGAAGGACAGTGTGCTTTGCTCTAGACAAAGTCTCCCATC 843
Db 781 AGCGACTGCATCCGACATAAAGAAACAGTTGTGCTCTGCCCCAACAAACAGGCGTCCCTTC 840
QY 844 CTTCCAGATGACAAACAGACGCATGCTGGGAGGCTGGCTGCTCTCTTCTCTGTG--CTG 900
Db 841 CTTCTGGATAACAAACAAAGACAGCGGAGGCTGGCTGCTCTCTCTGTCTGTCTG 900
QY 901 CTGTGGCTGTGTGGTGTGTCAGCTGGGATCTACCTAACTTGGAGGCAAGAAAGGAGC 960
Db 901 CTGGTGGCCACATGGTGTGCTGGTGGCAGGATCTATCTAATGTGGAGGCAAGAAAGGATC 960
QY 961 ACGAAGACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
Db 961 AAGAAGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1017
QY 1021 TATCTTCTGAGATATGTTTTCATACACCGCTCTGTGCGCTTCACTGACTTCTTCTTCAAAAC 1080
Db 1018 TACCCATCTGAATATGTTTTCATACACAAATTTGTACTTCACTGAATTTCTTCAAAAC 1077
QY 1081 TACTGAGAAGTGAGTGTATCTTTGAAATATGCGAGAAAAAGAAATCGCCAGATGGGG 1140
Db 1078 CATTCGAGAAGTGAGTGTATCTTTGAAAGTGGCAGAAAAAGAAATAGCAGATGGGT 1137
QY 1141 CCGGTACGTGGCTGACCACTCAGAACGACGCGGAGATAAGTGGTCTTCTTCTTCTTCTTCC 1200
Db 1138 CCAGTGCAGTGGCTTGGCACTCAAAAGAAAGGAGCAGACAAAGTGTCTTCTTCTTCTTCC 1197
QY 1201 AGTGACGCTCCGACCCCTTGTGACAGTGGCTGTGGCCACAATGAGGGCAGCGCCAGGGAG 1260
Db 1198 AATGAGCTCAACAGTGTGCGATGTACTGTGGCAAGAGCGGCGAGTCCCAAGTNG 1257
QY 1261 AACTCTCAGGATCTGTTCCTCTTGCCTTTAACTCTTTTGTAGTGAATTCAGAGCCAG 1320
Db 1258 AACTCTCAAGACTCTTCTCCCTCTTGCCTTTAACTCTTTCTGAGTGTCTAAGAAAGCCAG 1317
QY 1321 ACGCATCTGCAAAATACCTGTGTGTCTATCTTGGGGAGAGACCTCAAAAGGCACTAT 1380
Db 1318 ATTCTCTGCAAAATACCTGTGTGTGTCTATCTTGTAGAGATTTGATACAAAGACGATTAC 1377
QY 1381 AATGCGCTCAGTGTCTGCCCCCAATATCATCTCATGAGGAGCGCCACAGCTTTCACACA 1440
Db 1378 AATGCTCTCAGTGTCTGCCCCCAAGTACCACTCATGAGGATGCCACTGCTTCTGTGCA 1437
QY 1441 GAACTTCTCAAGCTACGAGAGCATGTTCAGTGAAGAAAACGCTCAAGCCCTGCCATGAT 1500
Db 1438 GAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCATCAAGCCCTGCCACGAT 1497
QY 1501 AGCTGTTACCCCTCTGTAG 1518
Db 1498 GGCCTGCTCTCTTGTAG 1515
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RESULT 13
US-10-175-737-399
; Sequence 399, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-399
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Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
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QY 13 CGGGCCATGTTGCTAGTGTGCTGATCTTGGCTGATCTGTCAGAGAGCGCCCTGCTCGA 72
Db 1 CGGGCGATGTGCTGCTGCTGCTAAAGCCTGCGCGCTGTGTCAGAGAGCGCCCTGATACCCGCA 60
QY 73 GAGCGGACTATTTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGGATGGTCAACAC 132
Db 61 GAGCGGACCGTTCAATGTGGCTCTGAAACTGGGCACTCCAGAGTGGATGCTACCAAT 120
QY 133 ACATCTACTCCAGGAGACTTTCAGGGACCTCCAAAGTGGAACTCGTCAAGACAAAGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTTCAGGGACCTCCAGTAGAAGCTGTTACAACTAGTGTGCA 180
QY 193 CGAGAGGATGTTTCAATTTTGTATGACATAAGCTGGATCTCCGGGCGAGACCCAGCATC 252
Db 181 ACAGGGGACTATTCAATTTTGTATGAACTGAGTGGGTACTCCGGGCGAGATGCCAGCATC 240
QY 253 CGCTTTGTAAGGGCCACCAAGATCTCGTGTAGTGGCAAAAAACAACATGAATTCATACAGC 312
Db 241 CGCTTTGTAAGGGCCACCAAGATTTGTGTAGGGCAAAAAAGCACTTCAGTCTCTACAGC 300
QY 313 TGTGTGAGGTGCAACTACACAGAGCGCTTCCAAAGCCAGACAGACCTTCCGGCGGCAAA 372
Db 301 TGTGTGAGGTGCAATTAACACAGAGCGCTTCCAGACTCAGACAGACCCCTCTGGTGTAAA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTATCAGCGCC 432
Db 361 TGGACATTTCTCTATCAGCGCTTCCCTGTAGAGCTGAAACAGAGTCTATTTTATTGGGGCC 420
QY 433 CATACATCTCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTGTGTGAATTCACC 492
Db 421 CATATATTTCTTAATGTCAAAATATGAATGAGATGGCCCTTTCATGTCTGTGNAATTCACC 480
QY 493 TCGCAGGCTGCTTAAACACAGTAAATGAATATAAAAAAGCAGTGCACCTGAGCGCGGAAGC 552
Db 481 TCACCAGGCTGCTTAGACCAACATTAATGAATATAAAAAAGTGTGTCAAGCGCGGAAGC 540
QY 553 CTGTGGGACCCAGACATCACTGCTTTGTAAGAAAGACGAGAGATGGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAACATCACTGCTTTGTAAAGAAAGATAGGAGACAGTAGAAGTGAATTC 600
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Qy	613	ACAACCAATCCCCTTGGAAACAGATACAGATTCTCATTTCAACGGGACAGACAAATTGGGG	672
Db	601	ACAACCAATCCCCTTGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGG	660
Qy	673	TTTTCTAGAGTGTGG-----AGAAATAACTGATGAGGAGCTGTGTAGCCATCCCG	723
Db	661	TTTTTCTCAGTGTTTGAGCCACACCAAGAAGAAACAAACGCGAGCTTCAGTGGTGAATTC	720
Qy	724	GTGACTGAGGAGAGTGAAGGTGGGTGTTACGTGACGCCCATATTTACATACCTCGCGC	783
Db	721	GTGACTGGGGATAGTGAAGTGTCTACGGTGCACTGTCTCATATTTCTTACTTGTGGC	780
Qy	784	AATGACTGCATCCGACGCGAAGGACAGTTGTCTTCTCAGACACAAAGTGTCCCATC	843
Db	781	AGCGACTGCATCCGACATAAAGGAAACAGTTGTCTCTGCCACAAACAGGCGTCCCTTTC	840
Qy	844	CTTCCAGATGACAAACAGACGATCTGCGGAGGCTGGCTCTCTCTCTGGTG---CTG	900
Db	841	CTCTCTGGATTAACAAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTCTCTCTCTCTG	900
Qy	901	CTGGTGGCTGTGTGGGTGTGGCAGCTGGGATCTACCTAACTTGGAGGCAAGGAAGGAGC	960
Db	901	CTGGTGGCCACATGGGTGTGTGGCAGGATCTATCTAATGTGGAGGCGCAAGGATC	960
Qy	961	ACGAAGACGTCTTTCTTCTTCCATATTTCCACATGTCTCTGCCCTCATTAAGTCTCTGGTGT	1020
Db	961	AAGAAGACTTCTTTTCTA---CCACCACACTACTGCCCTCCCTTCTGTGTGTGT	1017
Qy	1021	TATCTCTTCTGAGATATGTTTCCATACACACCGTCTCGCTCTCACTGACTTTCTTCAAAAC	1080
Db	1018	TAGCCCATCTGAATATGTTTCCATCACAAATTTGTACTTCTCACTGAATTTCTTCAAAAC	1077
Qy	1081	TACTGAGAGTGAAGTGTATCTTGAATAATGGCAGAAAAAGAAAAATCGCCGAGATGGG	1140
Db	1078	CATTGAGAAAGTGAAGTGTATCTTGAATAATGGCAGAAAAAGAAAAATAGCAGAGATGGT	1137
Qy	1141	CCGGTACAGTGGCTGACCACTCAGAAGCAAGCGGCAGATAAAGTGTCTTCTTCTTCCC	1200
Db	1138	CCAGTGGAGTGGCTTCCCACTCAAGAAGGCGACGACAAGTGTCTTCTTCTTCTTCC	1197
Qy	1201	AGTGAGTCCCGACCCCTTTGTGACAGTGCCTGTGGCCACAATAGGGGCGAGCCGAGGAG	1260
Db	1198	AATGAGTCAACAGTGTGTGCGATGCTACTGTGGCAGACGAGGGGCGAGTCCAGTGAG	1257
Qy	1261	AATCTCAGAGATCTGTTCCTCTTGCCCTTTAACTCTTTTGTAGTGAATTCAGCAGCCAG	1320
Db	1258	AACTCTCAAGACCTCTTCCCTCTTGCCTTTAACTCTTTTCTGCACTGTATTAAGAAGCCAG	1317
Qy	1321	ACGCATCTGCACAAATACCTGTGTGTCTATCTTGGGGAGCAGACCTCAAGGGGACTAT	1380
Db	1318	ATTTCATCTGCACAAATACGTGTGTGTCTACTTTAGAGAGATTGATCAAAAGACGATTAC	1377
Qy	1381	AATGCCCTGAGTGTCTGCCCCCAATATCATCTCATGAAGGAGCCACAGCTTTCCACACA	1440
Db	1378	AATGCTCTCAGTGTCTGCCCCCAAGTACCACTCATGAAGGATGCCATGCTTCTGTGCA	1437
Qy	1441	GAACTTCTCAAGGCTACGCAAGCATGTCAAGTGAAGAAACGCTCACAAAGCCTGCCATGAT	1500
Db	1438	GAACTTCTCCTCATGTCAAGCAGCAGGTGTTCAGCAGGAAAAAGATCACAAAGCCTGCCAGAT	1497
Qy	1501	AGCTGTTCCACCTTTGAG	1518
Db	1498	GGCTGTGTCTTTGAG	1515

RESULT 14

US-10-063-502-157

; Sequence 157, Application US/10063502

; Publication No. US20030023042A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvaroff, Ellen

```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,502
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-502-157

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Query Match 49.1%; Score 963.6; DB 9; Length 1515;

Best Local Similarity 78.7%; Pred. No. 3e-313;

Sequence	Matches	Mismatches	Indels	Gaps
Conservative	1194	0	15	3
Relaxed	1194	0	15	3

Qy	13	CGGGCCATGTTGCTAGTGGTCTGATCTTGGCTGCAATCGTGTGCAGGAGCGCCCTCGCTCGA	72
Db	1	CCGGCGATGTCGCTCGTGTCTAAAGCCTGGCCGCGTGTGCAGGAGCGCCGTACCCCGA	60
Qy	73	GAGCGCACTAATCAGTGTGGCTCTGAGACAGAGGCGCATCTCCAGAGTGGATGGTCCAAAC	132
Db	61	GAGCCGACCGTTCAATGTGGCTCTGAACCTGGGCCATCTCCAGTGGATGCTTACAAACAT	120
Qy	133	ACATCTACTCCAGGAGACTTTGAGGACCTCCAAAGTGGAACTCGCTCAAGACAAGTGTGGCA	192
Db	121	GATCTAATCCCGGAGACTTTGAGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCA	180
Qy	193	GCAGAGAGTGTTCATATTTTGTAGAACATAAGCTGGATACTCCGGGACAGCGCCAGCATC	252
Db	181	ACAGGGACTATTCAATTTTGTAGTAATGAAGCTGGGTATCTCCGGCGAGATGCCAGCATC	240
Qy	253	CGCTTGTGGAAGCCACCAGATCTCGGTGAGTGGCAAAACCAACATGAATTCATACAGC	312
Db	241	CGCTGTTGGAAGCCACCAGAATTTGTGTGAOCGGCAAAAGCAACTTCAGTCCCTACAGC	300
Qy	313	TGTGTAGGTGCAACTACACAGAGGCGCTTCCAAAGCCGACACAGACCTTCCGGCGGCAAA	372
Db	301	TGTGTAGGTGCAATTTACACAGAGGCGCTCCAGACTCAGACCAGACCCCTCTGGTGGTAA	360
Qy	373	TGGACATTTCTCTATGATGAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC	432
Db	361	TGGACATTTTCTTACATCGGCTTCCCTGTAGAGCTGAAACACAGCTATTCTTATTGGGGCC	420
Qy	433	CATACATCCCGAATGCTAATATGAATGAGGACAGCGCTTCTTGTCTGTGAATTCACC	492
Db	421	CATAAATATCCTAATGCAATATGAATGAAGATGGCGCTTCCATGCTGTGAATTTTACC	480
Qy	493	TCGCGAGGCTGCCTTAAACACGTAATGAAATATAAAAAGCAGTGCCTCAGCGCGGAAGC	552
Db	481	TCACGAGCTGCCTAGNCCACATAATGAATAATATAAAAAAGTGTCTCAAGCGCGGAAGC	540
Qy	553	CTGTGGGACCCAGACATCACTGCTTGTAAAAAGAAAGAGAGATGTTGAAAGTGAATTC	612
Db	541	CTGTGGGATCCGAACATCACTGCTTGTGAAGAAGAAATGAGGAGACAGTAGAAGTGAATTC	600
Qy	613	ACAACCAATCCCTTGGAAACAGATACAGATTCTCATTTCAACGGGACAGGACATTTGGGG	672
Db	601	ACAACCACTCCCTTGGGAAAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGG	660
Qy	673	TTTTTCTAGATGTGG-----AGATAAATCTGATGAGGACGCTGTGAGCCATCCCG	723
Db	661	TTTTTCTCAGGTGTTTGAGCCACACCCAGAGAAACAAACCGGAGCTTCAGTGGTGATCCA	720
Qy	724	GTGACTGAGGAGAGTGAAGGTGGCGGTGGTTTCAGCTGACGCCCATATTTACATACCTGCGGC	783

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Db 721 GTGACTGGGATAGTGAAGGTGCTACGGTGCAGCTCACTCATATTTCTACTTGTGC 780
Qy 784 AATGACTGCATCCGAGCGGAGGACAGTGTGCTTTGCTCGAGACAAGTGTCCCATC 843
Db 781 AGGACTGCATCCGATGAAGAAAGTGTGCTGTGCCCAACAAAGCGGTCCCTTC 840
Qy 844 CTCCAGATGACAAACAGACGCTGCTGGGAGGCTGCTGCTCTCTCTCTCTCTG 900
Db 841 CCTCTGATAAACAAGAACGACGCGGAGGCTGCTGCTCTCTCTCTCTCTCTG 900
Qy 901 CTGGTGGCTGTGTGGGTGCTGGGAGTCTACTAATCTGGAGCAAGAAAGGAC 960
Db 901 CTGGTGGCCACATGGGTGCTGGTGGGAGGATCTATCTAATGTGGAGGACGAAAGGATC 960
Qy 961 AGAAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Db 961 AGAAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
Qy 1021 TATCTCTCTGAGATATGTTTCCATCACACGCTGCTGCTCTCTCTCTCTCTCTCT 1080
Db 1018 TACCCATCTGAATATGTTTCCATCACACATTTGTTACTTCACTGAATTTCTTCAAAAC 1077
Qy 1081 TACTGAGAAGTGAAGTCTCTCTGAAAAATGSCAGAAAAAGAAATCCCGAGATGGG 1140
Db 1078 CATTCGAGAAGTGAAGTCTCTCTGAAAAAGTGGCAGAAAAAGAAATAGCAGAGATGGT 1137
Qy 1141 CCGGTACAGTGGCTGACCACTCAGAGCAAGCGGAGATAGAGTGTCTCTCTCTCTCT 1200
Db 1138 CAGTGCAGTGGCTTGGCCACTCAAAAGAGGAGGAGCAGACAAAGTGTCTCTCTCTCT 1197
Qy 1201 AGTGAGCTCCGACCCCTTTGTGACAGTGTCTGTGGCCACAATGAGGGAGCGCAGGAG 1260
Db 1198 AATGAGCTCAACAGTGTGTGCGATGTACTGTGGCAAGAGCGGAGTCCAGTGA 1257
Qy 1261 AACTCTCAGAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1258 AACTCTCAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1317
Qy 1321 AGCATCTGCACAAATACCTGTGTGTGTCTATCTTGGGGAGCAGACCTCAAGGCGACTAT 1380
Db 1318 ATTCTCTGCACAAATACCTGTGTGTGTCTATCTTGGGGAGCAGACCTCAAGGCGACTAT 1377
Qy 1381 AATGCCCTCAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCCACAGCTTTCCACACA 1440
Db 1378 AATGCTCTCAGTGTCTGCCCCCAAGTACACCTCATGAAGAGTGCACACTGCTTCTGTGCA 1437
Qy 1441 GAATCTCTCAAGCTACGAGAGCATGTCTGAGTGAAGAAAGCGTCAAGGCTGCGCATGAT 1500
Db 1438 GAATCTCTCAAGCTACGAGAGCATGTCTGAGTGAAGAAAGCGTCAAGGCTGCGCATGAT 1497
Qy 1501 AGCTGTTCAACCTCTGTAG 1518
Db 1498 GGCTGCTGCTCTCTGTAG 1515

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RESULT 15
US-10-173-706-399
; Sequence 399, Application US/10173706
; Publication No. US2003022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-706-399

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

Qy 13 CGGCGCATGTTGCTAGTGTGCTGATCTTGGCTGATCTGTGAGGAGCGCCCTGCTCGA 72
Db 1 CGGCGCATGTCGCTGCTGCTAGCCCTGCTAGCCCTGCGCGGCTGTGCGAGGAGCGCGTACCCGA 60
Qy 73 GAGCGGACCTATTTCAGTGTGGCTCTGAGACAGGCGCATCTCCAGAGTGGATGTCCTCAACAC 132
Db 61 GAGCGGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTCAACAAT 120
Qy 133 ACATCTACTCCAGGAGACTTGGAGGACCTCCAAGTGGAACTCGTCAAGACAAGTGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAACCTGTTTACAACCTAGTGTGCA 180
Qy 193 CGAGGAGGTTTTCATTTTGTATGAACATAAGCTGGATCTCCGGGAGAGCGCCAGCATC 252
Db 181 ACAGGGGACTATTCAATTTTGTATGAATGTAAAGTGGGTACTCCGGGAGAGTGCACGATC 240
Qy 253 CGTTGTTGAAGGCGCCCAAGATCTCGTGTAGTGGCAAAAAACAATCAATTTTATACAGC 312
Db 241 CGTTGTTGAAGGCGCCCAAGATTTGTGTAGGCGCAAAAGCACTTCCAGTCTTACAGC 300
Qy 313 TGTGTAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGCGGCAAA 372
Db 301 TGTGTAGGTGCAATTAACACAGAGGCTTCCAGACTCAGACAGACCTCTGGTGTGTA 360
Qy 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGTGGACACTCTCTATCTCATAGCGCC 432
Db 361 TGGACATTTCTCTATGTAGGCTTCCCTGTAGAGTGGAAACAGACTCTATTTTCAATTTGGG 420
Qy 433 CATTAACATCCCAATGTATTAATGAATGAGCAGACGCTCTTTGCTGTGTAACCTTACC- 492
Db 421 CATTAATTTCTTAATGAATAATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACC 480
Qy 493 TCGCAGGCTGCCTAAACCAAGTAAATGAATATAAAGAGCAGTGCACCTGAGGCGGGAAGC 552
Db 481 TCACAGGCTGCCTAGACCAATTAATGAATATAAAGAGTGTGTCAAGGCGGGAAGC 540
Qy 553 CTGTGGGAGCCAGACATCATCTGCTTTGTAAAGAACGAGAAAGATGGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAAACATCATCTGCTTTGTAAAGAAAGTGAAGAGACAGTAGAAGTGAATTC 600
Qy 613 ACAACCAATCCCTTGGAAACAGATACAGATTTCTTATTCAACGGGACACGACATTTGGG 672
Db 601 ACAACCACTCCCTGGGAAACAGATACATGCTCTTATCCAAACAGACACTATCATCGG 660
Qy 673 TTTTCTAGAGTGTGG-----AGAAATAACTGATGAGGAGCTGTGTAGCCATCCG 723
Db 661 TTTTCTCAGGTGTTTGAGCCACACCAAGAAAGAAACAAACGCGAGCTTTCAGTGGTATTCCA 720
Qy 724 GTGACTGAGGAGAGTGAAGTGGGTGCTGAGTGCACCTTACATTTTACATACCTTGGCGC 783
Db 721 GTGACTGAGGAGTGAAGTGGTGTACCGTGCAGCTGACTCCATATTTTCTTACTTGTGGC 780
Qy 784 AATGACTGCATCCGAGCGGAGGACAGTGTGCTTTGCTCTCAGAGACAAGTGTCTCCCATC 843
Db 781 AGGACTGCATCCGACATATAAGGAAACAGTGTGCTCTGCCCCCAACAAAGGCGTCCCTTTC 840
Qy 844 CTCCAGATGACAAACAGACGATCTGCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTG 900

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:31:59 ; Search time 65.2562 Seconds
(without alignments)
9225.277 Million cell updates/sec

Title: US-09-778-971-3
Perfect score: 1963
Sequence: 1 gtcgcaatggccggccat.....aaaaaaaaaaaaaaaaaaaaa 1963

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.2	2.3	3223	2	US-08-620-694A-9
2	44.2	2.3	3223	3	US-09-022-255-9
3	44.2	2.3	3223	3	US-09-022-696-9
4	44.2	2.3	3223	3	US-08-978-773-3
5	44.2	2.3	3223	3	US-09-022-253-9
6	44.2	2.3	3223	3	US-09-022-260-9
7	44.2	2.3	3223	3	US-09-022-259-9
8	44.2	2.3	3223	4	US-09-022-257-9
9	38	1.9	1364	2	US-08-872-302-3
10	37.4	1.9	1697	4	US-09-346-408-5
11	37.4	1.9	7218	1	US-08-232-463-14
12	37.2	1.9	2413	4	US-09-518-046-1
13	37.2	1.9	2416	4	US-09-518-046-1
14	37.2	1.9	2544	4	US-09-518-046-3
15	36.2	1.8	807	4	US-09-715-994-3
16	36	1.8	756	2	US-08-530-165-1
17	35.8	1.8	2815	1	US-08-230-491A-1
18	35.8	1.8	2815	1	US-08-619-280A-1
19	35.8	1.8	2815	2	US-08-940-391-1
20	35.2	1.8	6909	2	US-08-804-196-1
21	35.2	1.8	6909	3	US-08-658-340-1
22	35.2	1.8	6909	3	US-08-746-111-26
23	34.6	1.8	2790	3	US-08-718-661-1
24	34.4	1.8	500	3	US-09-141-000-2
25	34.4	1.8	7218	1	US-08-232-463-14
26	34.2	1.7	2311	4	US-09-624-691A-14
27	34	1.7	885	3	US-08-651-136C-23

c	28	34	1.7	885	4	US-09-229-911A-23	Sequence 23, Appl
c	29	34	1.7	2073	4	US-09-221-017B-404	Sequence 404, Appl
	30	34	1.7	2226	3	US-08-951-260A-1	Sequence 1, Appl
	31	33.8	1.7	1740	1	US-08-362-512A-3	Sequence 3, Appl
	32	33.8	1.7	1740	4	US-08-964-939-3	Sequence 3, Appl
c	33	33.8	1.7	5697	3	US-08-814-052-11	Sequence 11, Appl
c	34	33.8	1.7	5697	3	US-08-812-829-11	Sequence 11, Appl
	35	33.6	1.7	1264	2	US-08-758-621-13	Sequence 13, Appl
	36	33.6	1.7	1264	4	US-09-107-858-13	Sequence 13, Appl
	37	33.6	1.7	4868	1	US-08-139-937-12	Sequence 12, Appl
	38	33.6	1.7	4868	5	PCT-US93-11310-12	Sequence 12, Appl
	39	33.6	1.7	8789	1	US-08-328-254-5	Sequence 5, Appl
	40	33.6	1.7	10136	1	US-08-353-700-2	Sequence 2, Appl
	41	33.6	1.7	10136	5	PCT-US95-16216-2	Sequence 2, Appl
	42	33.4	1.7	501	4	US-09-326-039-4	Sequence 4, Appl
	43	33.4	1.7	1279	4	US-09-277-716-31	Sequence 31, Appl
	44	33.4	1.7	1279	4	US-09-609-161B-31	Sequence 31, Appl
	45	33.4	1.7	1313	4	US-09-149-476-112	Sequence 112, Appl

ALIGNMENTS

RESULT 1
US-08-620-694A-9
; Sequence 9, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTL8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
; US-08-620-694A-9

Query Match      2.3%; Score 44.2; DB 2; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGAATGTTCAACACACACTCACTCAGAGAGACTTGAGGACCTCAAGTGGAACTCGTC 177
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 TGGATTCAACCTCGAAACCTGACCCCTCTCCCAAGGACCTGCAGATCCAGCTGCAC 335
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 AAGCAAGTGTGGCAGCAGAGAGTGTTCATTTTGTATGAACATAAGCTGGATCTCGG 237
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 TTGCCCCACACCAACCAAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 GCAGACGCCAGCATCCGCTTGTGAAGGCCACCAAGATCTCGGTGAGTGGCAAAACAC 297
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 ACAGACGCCAGCATCCCTGTACTCGAGGGTGCAGAGTTATCTGT-----C 440
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCA 357
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 CTGAGCTGAACACCAATGAACGTTTGTGCGTACAGTTTGTCTCCTCAAACTGAGG 500
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 CTTCCCGCGGCAAAATGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTC 417
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 CATCACACACAGCGGTGGCGTTTACCTTCAGCCACATTTGTGGTTGACCTGACCCAGGAA 560
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 TATCTCATCAGGCCCAATAACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTG 477
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
561 TATGAGGTGACCGTTTCCACCTGCCCAAGCCCATCCCTGTATGGGGACCCAAACAC 620
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 478 TCTGTGAATCTCACCTCGCCAGGCTGCCCTAAACCAACCACTAATGAATAATAAAGCAGTGC 537
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
621 TCCAAGAAATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGTAAACCGCCATGC 680
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 538 ACTGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTATAAAGACAGAGATG 597
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
681 ATGAGCTCAGGCAGCCTGTGGGACCCCAACATCACTCCGTGGAGACCTCTGGAGCCCA 740
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 598 GTTGAAGTGAATTTTAC 614
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
741 CTGCGTGTGAGCTTAC 757
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query Match      2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGGATGTGTCACACACACTCACTCAGGAGACTTTGAGGGACCTCCAAAGTGGAACTCGTC 177
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 TGGATTCAACCTCGAAACCTGACCCCTCTCCCAAGGACCTGCAGATCCAGCTGCAC 335
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 AAGCAAGTGTGGCAGCAGAGAGTGTTCATTTTGTATGAACATAAGCTGGATCTCGG 237
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 TTGCCCCACACCAACCAAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 GCAGACGCCAGCATCCGCTTGTGAAGGCCACCAAGATCTCGGTGAGTGGCAAAACAC 297
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 ACAGACGCCAGCATCCCTGTACTCGAGGGTGCAGAGTTATCTGT-----C 440
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCA 357
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 CTGAGCTGAACACCAATGAACGTTTGTGCGTACAGTTTGTCTCCTCAAACTGAGG 500
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 CTTCCCGCGGCAAAATGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTC 417
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 CATCACACAGCGGTGGCGTTTATCCTTCAGCCATTTGTGTTGACCTGACCAAGGAA 560
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 TATCTCATCAGGCCCAATAACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTG 477
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
561 TATGAGGTGACCGTTTCCACCTGCCCAAGCCCATCCCTGTATGGGGACCCAAACAC 620
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 478 TCTGTGAATCTCACCTCGCCAGGCTGCCCTAAACCAACCACTAATGAATAATAAAGCAGTGC 537
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
621 TCCAAGAAATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGTAAACCGCCATGC 680
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 538 ACTGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTATAAAGACAGAGATG 597
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
681 ATGAGCTCAGGCAGCCTGTGGGACCCCAACATCACTCCGTGGAGACCTCTGGAGCCCA 740
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 598 GTTGAAGTGAATTTTAC 614
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
741 CTGCGTGTGAGCTTAC 757
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

US-09-022-255-9
Sequence 9, Application US/0902255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
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RESULT 3

US-09-022-696-9
; Sequence 9, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTLA8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693

US-09-022-696-9

Query Match 2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGGATGGTCCACACACACTCACTCAGAGACTTGAGGAGCTCCCAAGTGGACTCGTC 177

DB 276 TGAATTCACCTCGAACTGACCCCTCTCCCAAGAGCTCGAGATCCAGCTGCAC 335

QY 178 AAGACAAGTGTGGCAGCAGGAGTTTTCATATTTTATGAACATAGCTGGATATCTCCGG 237

DB 336 TTGCGCCACACCCACAGAGACCTGTTCCCGGTGGCTCACATCGAATGGACACTGGAG 395

QY 238 GCAGACGCCAGCATCGCTTGTGTAAGGCCACCAAGATCTGCGTGAAGTGGCAAAACAC 297

DB 396 ACAGAGCGCAGCATCTGTACCTCGAGGTGCAGAGTTATCTGT-----C 440
QY 298 ATGAATTCATACAGCTGTGTAGAGTGCAACTACACAGAGGCCTTCCAAAGCCAGACCA 357
DB 441 CTGCAGCTGAACCAATGAAGCTTTGTGCGCTGAGTTTGTCTGTCCAACTGAGG 500
QY 358 CTTCCGCGGGCAAAATGGACATCTCCTATGTAGGCTTCCCTGTGTAGAGCTGAGCACTTC 417
DB 501 CATCACACAGCGGTGGCGTTTACCTTCAGCCACTTTGTGTTGACCTTGACCCAGGAA 560
QY 418 TATCTCATCAGCGCCCAATACATCCCAATGCTATATGAATGAGGACAGCCCTTCTTTG 477
DB 561 TATGAGGTGACCGTTTACCCCTGCGCAAGCCCATCCCTGATGGGACCCCAAAACCCAG 620
QY 478 TCTGTGAACCTTCACCTCGCCAGCTGCCTTAAACACAGTAATGAAATATATAAAGCAGTGC 537
DB 621 TCCAAGATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGTAAACCGCCATGC 680
QY 538 ACTGAGCGGGAAAGCTGTGGAGCCAGACATCACTGTGTTTAAAAAGAACGAGAGATG 597
DB 681 ATGAGCTCAGGAGCGCTGTGGAGCCCAACATCACCGTGGAGACCTTGAGGCCCAACCAG 740
QY 598 GTTGAAGTGAATTCAC 614
DB 741 CTGCGTGTGAGCTTCAC 757

RESULT 4

US-08-978-773-3
; Sequence 3, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IL-17R
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2690
US-08-978-773-3

Query Match 2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;
QY 118 TGGATGTCACACACACACTCACTCCAGGAGACTTCAGGAGCCTCCAAAGTGAACCTCGTC 177
DB 276 TGGATTCACCTCGAAACCTGACCCCTCTCTCCCAAGGACCTGCAGATCCAGCTGCAC 335
QY 178 AGACAAAGTGTGGCAGAGAGAGTTTCAATTTTGAAGCAATGAAGCTGGATACCTCCGG 237
DB 336 TTTGCCACACACCCCAACAAAGAGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
QY 238 GCAGAGCCGAGCATCCGCTTGTGAGGCCACCAAGATCTGGTGAAGTGGCAAAACACAC 297
DB 396 ACAGAGCCGAGCATCTGTACCTCGAGGGTGCAGAGTTATCTGT-----C 440
QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGCCCTTCCAAAGCCAGACAGA 357
DB 441 CTGCAGCTGAACACCAATGAACGTTTGTGCGTCAGGTTTGAGTTTCTGTCTCAACTGAGG 500
QY 358 CTTCCGGCGGGAATGAGCACTTCTCTATGAGGCTTCCCTGTGAGCTGAGCACTCTC 417
DB 501 CATCACACAGCGGTGGGGTGTTCACCTTCAGCCACTTGTGCTTACCTGACCCAGGAA 560
QY 418 TATCTCATCAGCGCCCATACATCCCAATGCTAATATGAATGAGCAGAGCCCTTCTTTG 477
DB 561 TATGAGTGACCGTTTACCTCGCCAGCCCTCCCAAGCCCATCCCTGATGGGACCCCAACAC 620
QY 478 TCTGTGAATTCACCTCGCCAGGCTGCCTAAACCAAGTATGAATATAAAGAGAGATG 597
DB 681 ATGAGCTCAGGAGCCCTGTGGGACCCCAACATCACCTGGAGACCCCTGGAGGCCAC 740
QY 598 GTTGAAGTGAATTTTAC 614
DB 741 CTGCGTGTGAGCTTTCAC 757

RESULT 5

US-09-022-253-9
Sequence 9, Application US/0902253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.253

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2693
US-09-022-253-9

Query Match 2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;
QY 118 TGGATGTCACACACACTCACTCCAGGAGACTTCAGGAGCCTCCAAAGTGAACCTCGTC 177
DB 276 TGGATTCACCTCGAAACCTGACCCCTCTCTCCCAAGGACCTGCAGATCCAGCTGCAC 335
QY 178 AAGCAAGTGTGGCAGCAGAGAGTTTCAATTTTGAATGAACATAAGCTGATCTCCGG 237
DB 336 TTTGCCACACACCCCAACAAAGAGAGCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
QY 238 GCAGAGCCGAGCATCCGCTTGTGAGGCCACCAAGATCTCGTGAAGTGGCAAAACACAC 297
DB 396 ACAGAGCCGAGCATCTGTACCTCGAGGGTGCAGAGTTATCTGT-----C 440
QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGCCCTTCCAAAGCCAGACAGA 357
DB 441 CTGCAGCTGAACACCAATGAACGTTTGTGCGTCAGGTTTGAGTTTCTGTCTCAACTGAGG 500
QY 358 CTTCCGGCGGCAATGAGCACTTCTCTATGAGGCTTCCCTGTGAGCTGAGCACTCTC 417
DB 501 CATCACACAGCGGTGGGGTGTTCACCTTCAGCCACTTGTGCTTACCTGACCCCTGACCA 560
QY 418 TATCTCATCAGCGCCCATACATCCCAATGCTAATATGAATGAGCAGAGCCCTTCTTTG 477
DB 561 TATGAGTGACCGTTTACCTCGCCAGCCCTCCCAAGCCCATCCCTGATGGGACCCCAACAC 620
QY 478 TCTGTGAATTCACCTCGCCAGGCTGCCTAAACCAAGTATGAATATAAAGAGAGATG 597
DB 681 ATGAGCTCAGGAGCCCTGTGGGACCCCAACATCACCTGGAGACCCCTGGAGGCCAC 740
QY 598 GTTGAAGTGAATTTTAC 614

Db	741	CTGCGTGTGAGCTTCAC	757
QY	238	GCAGAGCCAGCATCCGCTTGTGTAAGGCCACCAAGATCTCGTGAAGTGGCAAAACAC	299
Db	396	ACAGAGCCAGCATCTGTACTCGAGGTCAGAGTTATCTGT	440
QY	298	ATGAATTCATACAGCTGTGTGAGTGCAACTACACAGAGGCTTCCAAAGCCAGACACAGA	357
Db	441	CTGCAGCTGAACACCAATGAACGTTTGTGGGTTCAGGTTTGTGTTCTGTCTCAAACTGAGG	500
QY	358	CCTTCCGGGGCAAAATGACATCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTC	417
Db	501	CATCACACAGGCGGTGGCGTTTACCTTCAGCCACCTTCCTGTATGAAATGAGGAGCCCTTCTTTG	477
QY	418	TATCTCATCAGCGCCCAATACATCCCCCAATGCTAATATGAATGAGGAGCCCTTCTTTG	477
Db	561	TATGAGTGACCGTTTACCAACCTGCCCAAGCCCATCCCTGATGGGACCCCAACACACAG	620
QY	478	TCTGTGAACCTTACCTCGCCAGGCTGCCTAAACCAACGTAATGAATATAAAAGAGTGC	537
Db	621	TCCAAGAAATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGGTAAACCCGCGCATGC	680
QY	538	ACTGAGGCGGGAAGCCTGTGGAGCCACAGACATCACTCTTGTAAAAAGAACGAGAATG	597
Db	681	ATGAGCTCAGGAGCCTGTGGACCCCAACATCACCTGTGAGAGCCCTGGAGCCACACAG	740
QY	598	GTTGAAGTGAATTTCCAC	614
Db	741	CTGCGTGTGAGCTTCAC	757
RESULT 7			
US-09-022-260-9			
; Sequence 9, Application US/09022260			
; Patent No. 6100235			
; GENERAL INFORMATION:			
; APPLICANT: Yao, Zhengbin			
; APPLICANT: Spriggs, Melanie			
; APPLICANT: Fanslow, William			
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17			
; NUMBER OF SEQUENCES: 10			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Immunex Corporation			
; STREET: 51 University Street			
; CITY: Seattle			
; STATE: WA			
; COUNTRY: USA			
; ZIP: 98101			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: Apple Power Macintosh			
; OPERATING SYSTEM: Apple Operating System 7.5.5			
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/022,260			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/620,694			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: USSN 08/410,535			
; FILING DATE: 23 MARCH 1995			
; CLASSIFICATION:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Perkins, Patricia Anne			
; REGISTRATION NUMBER: 34,695			
; REFERENCE/DOCKET NUMBER: 2617-B			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (206)587-0430			
; TELEFAX: (206)			
; INFORMATION FOR SEQ ID NO: 9:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 3223 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA to mRNA			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; ORIGINAL SOURCE:			
; ORGANISM: Human			
; STRAIN: IL-17 R (hCTL8 receptor)			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 93...2693			
US-09-022-260-9			
Query Match 2.3%; Score 44.2; DB 3; Length 3223;			
Best Local Similarity 45.1%; Pred. No. 0.008;			

LENGTH: 3223 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORGANISM: Human
 STRAIN: IL-17 R (hCTL8 receptor)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 93..2693
 US-09-022-259-9

Query Match 2.3%; Score 44.2; DB 4; Length 3223;
 Best Local Similarity 45.1%; Pred. No. 0.008;
 Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGGATGGTCCACACACACTCACTCCAGGAGACTTGGAGGACCTCCAAAGTGGAACTCGTC 177
 DB 276 TGGATTCACCTCGAACCTGACCTCTCCCAAGGACCTGAGATCCAGCTGCAC 335
 QY 178 AGACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGAATGAACATAAGCTGGATACCTCGG 237
 DB 336 TTTGCCACACACCAAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
 QY 238 GCAGAGCCGAGATCCGCTGTTTGAAGGCCACCAAGATCTGCTGAGTGGCAAAACACAC 297
 DB 396 ACAGAGCCGAGATCTGACTCTCGAGGCTGAGGTTTCTGT-----C 440
 QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACACAGA 357
 DB 441 CTGACGTGAACACCAATGAACGTTTGTGGTCAGGTTTGTCTGTCTGCTCAACCTGAGG 500
 QY 358 CCTTCGGGGGCAATGAGACATCTCTATGTAGGTTCCCTGCTGGAGCTGAGCACTCTC 417
 DB 501 CATCACACAGCGGTGGCGTTTACCTTCAGCCACTTTGTGGTTGACCTGACCCAGGAA 560
 QY 418 TATCTCATCAGCGCCCAATACATCCCAATGCTTAATGAATGAGGACAGCCCTTCTTTG 477
 DB 561 TATGAGGTGACCGTTTCACTCCCAAGGCCATCCCTGATGGGGACCCCAACACCCAG 620
 QY 538 ACTGAGCGGGAGCTGTGGGACCCAGACATCACTGCTTTGTAAGAAAGACAGAGATG 597
 DB 681 ATGAGCTCAGGAGCGCTGTGGGACCCCAACATCAGCTGGAGACCTGGAGGCCACCAG 740
 QY 598 GTTGAAGTGAATTTTAC 614
 DB 741 CTGCGTGTGAGCTTAC 757

RESULT 8
 US-09-022-257-9
 Sequence 9, Application US/09022257
 Patent No. 6197525
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022.257
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/410,535
 FILING DATE: 23 MARCH 1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3223 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN: IL-17 R (hCTL8 receptor)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 93..2693
 US-09-022-257-9

Query Match 2.3%; Score 44.2; DB 4; Length 3223;
 Best Local Similarity 45.1%; Pred. No. 0.008;
 Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGGATGGTCCACACACACTCACTCCAGGAGACTTGGAGGACCTCCAAAGTGGAACTCGTC 177
 DB 276 TGGATTCACCTCGAACCTGACCTCTCCCAAGGACCTGAGATCCAGCTGCAC 335
 QY 178 AGACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGAATGAACATAAGCTGGATACCTCGG 237
 DB 336 TTTGCCACACCAAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
 QY 238 GCAGAGCCGAGATCCGCTGTTTGAAGGCCACCAAGATCTGCTGAGTGGCAAAACACAC 297
 DB 396 ACAGAGCCGAGATCTGACTCTCGAGGCTGAGGTTTCTGT-----C 440
 QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACACAGA 357
 DB 441 CTGACGTGAACACCAATGAACGTTTGTGGTCAGGTTTGTCTGTCTGCTCAACCTGAGG 500
 QY 358 CCTTCGGGGGCAATGAGACATCTCTATGTAGGTTCCCTGCTGGAGCTGAGCACTCTC 417
 DB 501 CATCACACAGCGGTGGCGTTTACCTTCAGCCACTTTGTGGTTGACCTGACCCAGGAA 560
 QY 418 TATCTCATCAGCGCCCAATACATCCCAATGCTTAATGAATGAGGACAGCCCTTCTTTG 477
 DB 561 TATGAGGTGACCGTTTCACTCCCAAGGCCATCCCTGATGGGGACCCCAACACCCAG 620
 QY 478 TCTGTGAACCTCACCTCGCCAGGCTGCTTAAACCCAGCTTAATGAATATAAAAGCAGTGC 537
 DB 621 TCCAGAAATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGTAACACCGCATGC 680

QY 538 ACTGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTTGTAATAAAGAACGAGAGATG 597
Db 681 ATGAGCTCAGGAGCAGCTGTGGGACCCCAACATCACCGTGAGACCCCTGGAGGCCACCCAG 740
QY 598 GTTGAAGTGAATTTCAC 614
Db 741 CTGCGTGTGAGCTTCAC 757

RESULT 9
US-08-872-302-3
; Sequence 3, Application US/08872302
; Patent No. 5846784
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. duPont de Nemours and Co.
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,302
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R
; REGISTRATION NUMBER: P-41,173
; REFERENCE/DOCKET NUMBER: BB-1084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1364 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1254
US-08-872-302-3

Query Match 1.9%; Score 38; DB 2; Length 1364;
Best Local Similarity 71.4%; Pred. No. 0.33;
Matches 50; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1894 TTTTGTAACTTTTAACTCTGTTAATCAATAATCCGTTTGGGAAGCTCTCAAAAAAAAAA 1953
Db 1288 TTTTGTAACTTTTGTAACTAATAATAATAATCTTGAATGAAGATAAAAAAAAAA 1347
QY 1954 AAAAAAAAAA 1963
Db 1348 AAAAAAAAAA 1357

RESULT 10
US-09-346-408-5
; Sequence 5, Application US/09346408B
; Patent No. 6338966
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Anderson, Shawn

; APPLICANT: Falco, Carl
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
; FILE REFERENCE: BB-1167-A
; CURRENT APPLICATION NUMBER: US/09/346,408B
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: 60/092,833
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Glycine max
US-09-346-408-5

Query Match 1.9%; Score 37.4; DB 4; Length 1697;
Best Local Similarity 64.4%; Pred. No. 0.56;
Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1877 ATGCTGCAGTAGACCGTTTGTAACTTTTAACTCTGTTAATCAATAATCCGTTTGGGAA 1936
Db 1609 ATACTTCAGGAGGATCCTCTGSCCAATCTAATAATAATAATAATAATAATAATAATA 1668
QY 1937 GCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963
Db 1669 GGCAAAAAAAAAAAAAAAAAAAAAA 1695

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-F1s
US-08-232-463-14

Query Match 1.9%; Score 37.4; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred. No. 1.2;
Matches 14; Conservative 209; Mismatches 170; Indels 0; Gaps 0;

Qy 511 CAGCTAATGAAATATAAAGACAGTGCAGCTAGGCGGAGCCTGTGGACCGACGACATC 570
Db 1435 CRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1376

Qy 571 ACTGCTTTAAAGAACGACGAGATGGTTGAAGTGAATTCACAAACCAATCCCTTGA 630
Db 1375 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1316

Qy 631 AACAGATACAGATTCATTCACCGGACGACGACATCGGGTTTCTAGAGTGTGGAG 690
Db 1315 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1256

Qy 691 AATAAACTGATGAGGAGCTGTGAGCCATCCCGGTGACTGAGGAGTGAAGTGGGTG 750
Db 1255 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1196

Qy 751 GTTCAGCTGACCCCATATTTACATACCTCGGCAATGACTGCATCCGACGCGGACGA 810
Db 1195 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1136

Qy 811 GTTGCTTTCTCAGACAGAGTGTCCATCCCTCCAGATGACACAGACGATGCTG 870
Db 1135 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1076

Qy 871 GGAGGCTGCTGCTCTCTCTCTCTGCTGCTGCTG 903
Db 1075 RRRRRRRATCGAAGCTCCCTCGACCTGCAG 1043

RESULT 12
US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1

Query Match 1.9%; Score 37.2; DB 4; Length 2413;
Best Local Similarity 63.3%; Pred. No. 0.77;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1874 TCTATGCTGCAGTACCGTTTGTAACTTTTAACTGTTAATGTAATGTAATGTTGG 1933
Db 2313 TCTTTGTAGCATTTGGTGTGACGTATTATTGCTTTGATTCCTCAATAATATGTTCC 2372

Qy 1934 GAAGCTCTCAAAAAAATAAAAAA 1963
Db 2373 TTCCCTCAAAAAAATAAAAAA 2402

RESULT 13
US-09-261-416-1
; Sequence 1, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1

Query Match 1.9%; Score 37.2; DB 4; Length 2416;
Best Local Similarity 63.3%; Pred. No. 0.77;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1874 TCTATGCTGCAGTACCGTTTGTAACTTTTAACTGTTAATGTAATGTAATGTTGG 1933
Db 2316 TCTTTGTAGCATTTGGTGTGACGTATTATTGCTTTGATTCCTCAATAATATGTTCC 2375

Qy 1934 GAAGCTCTCAAAAAAATAAAAAA 1963
Db 2376 TTCCCTCAAAAAAATAAAAAA 2405

RESULT 14
US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3

Query Match 1.9%; Score 37.2; DB 4; Length 2544;
Best Local Similarity 63.3%; Pred. No. 0.79;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1874 TCTATGCTGCAGTACCGTTTGTAACTTTTAACTGTTAATGTAATGTAATGTTGG 1933
Db 2444 TCTTTGTAGCATTTGGTGTGACGTATTATTGCTTTGATTCCTCAATAATATGTTCC 2503

Qy 1934 GAAGCTCTCAAAAAAATAAAAAA 1963
Db 2504 TTCCCTCAAAAAAATAAAAAA 2533

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Search completed: May 28, 2003, 10:22:39
Job time : 118.256 secs

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XX 04-FEB-2000; 2000US-0180374.
PR (UYAR-) UNIV ARKANSAS.
PA Shaughnessy JD;
PI WPI; 2001-496920/54.
DR P-PSDB; AAE07162.
XX
PT New nucleic acids encoding an interleukin (IL)-17 receptor related
XX protein for use as a marker for leukemia
XX
XX Claim 1a; Page 76-77; 87bp; English.
XX
CC The present sequence is a cDNA encoding mouse interleukin (IL)-17
CC receptor related protein (Evi27). Mouse Evi27 gene was mapped to
CC chromosome 14. Evi27 is a common site of retroviral integration
CC in BKH murine myeloid leukaemias. Evi27 cDNA sequences are useful
CC as antisense molecules to inhibit Evi27 protein or for chromosomal
CC mapping or mutational analysis of Evi27 protein. They are proviral
CC integration sites associated with leukaemias and monitoring this
CC site provides a genetic tag for disease gene identification. The
CC proteins of the invention are useful to stimulate the secretion of
CC proinflammatory cytokines such as IL-8 and plays an important role
CC in the developmental and/or disease processes of haematopoietic
CC cells. Hence modulating the expression of Evi27 at the RNA or
CC protein level is used in the treatment of diseases such as cancer
CC or autoimmune diseases.
XX
SQ Sequence 1963 BP; 510 A; 492 C; 494 G; 467 T; 0 other;
Query Match 100.0%; Score 1963; DB 22; Length 1963;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCCAGTGGCCGCGCATTTGCTAGTGTGCTGATCTTGCTGCATCGTGCAGAGC 60
DB 1 GTGGCCAGTGGCCGCGCATTTGCTAGTGTGCTGATCTTGCTGCATCGTGCAGAGC 60
QY 61 GCCCTGCTGAGAGCGCGACTATTCACTGTGCTGTGAGACAGGGCCATCTCCAGATGG 120
DB 61 GCCCTGCTGAGAGCGCGACTATTCACTGTGCTGTGAGACAGGGCCATCTCCAGATGG 120
QY 121 ATGCTCCACACACTCACTCCAGAGACTTGAGGAGACCTCCAAAGTGAATCGTCAAG 180
DB 121 ATGCTCCACACACTCACTCCAGAGACTTGAGGAGACCTCCAAAGTGAATCGTCAAG 180
QY 181 ACAAGTGTGACAGAGAGATTTCATTTTGAATGAACAATAAGCTGATATCTCCGGCA 240
DB 181 ACAAGTGTGACAGAGAGATTTCATTTTGAATGAACAATAAGCTGATATCTCCGGCA 240
QY 241 GAGGCCAGCATCGCTTTGTGAAGGCCACAAAGATCTGCTGAGTGCAGAAAACAATG 300
DB 241 GAGGCCAGCATCGCTTTGTGAAGGCCACAAAGATCTGCTGAGTGCAGAAAACAATG 300
QY 301 AATTTCATACAGCTGTGTGAGGTGCACTACAGAGGCTTCCAAAGCCAGACCAAGCT 360
DB 301 AATTTCATACAGCTGTGTGAGGTGCACTACAGAGGCTTCCAAAGCCAGACCAAGCT 360
QY 361 TCCGGCGGCAATGACATTTCTCTATGTAGGCTTCCCTGTGAGAGCTGACACTCTAT 420
DB 361 TCCGGCGGCAATGACATTTCTCTATGTAGGCTTCCCTGTGAGAGCTGACACTCTAT 420
QY 421 CTGATCAGCGCCCAATACATCCCAATGCTAATATGATAGAGACAGCCCTTTGTCT 480
DB 421 CTGATCAGCGCCCAATACATCCCAATGCTAATATGATAGAGACAGCCCTTTGTCT 480
QY 481 GTGAACCTTCACTCGCAGGCTGCTAAACAGTAAATGAATTAATAAGAGAGTACT 540
DB 481 GTGAACCTTCACTCGCAGGCTGCTAAACAGTAAATGAATTAATAAGAGAGTACT 540
QY 541 GAGCGGGAAGCTGTGGAGCCAGACATCATGCTTTGAAAAAGAGAGAGATGTT 600

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DB 541 GAGCGGGAAGCTGTGGAGCCAGACATCATGCTTTGAAAAAGAGAGAGATGTT 600
QY 601 GAAGTAATTTCAACACCAATCCCTTTGAAAACAGATAACGATTTCTATTACGGGAC 660
DB 601 GAAGTAATTTCAACACCAATCCCTTTGAAAACAGATAACGATTTCTATTACGGGAC 660
QY 661 ACACATATGGGGTTTTCTAGAGTGTGAGAAATAAATGATGAGAGAGCTGTAGCATC 720
DB 661 ACACATATGGGGTTTTCTAGAGTGTGAGAAATAAATGATGAGAGAGCTGTAGCATC 720
QY 721 CCGGTACTGAGAGAGTGAAGTGGGTGTTGACTGATACCCCATATTTACATACCTGC 780
DB 721 CCGGTACTGAGAGAGTGAAGTGGGTGTTGACTGATACCCCATATTTACATACCTGC 780
QY 781 GGAATGACTGATCCGAGCGGAGGAGAGATTTGCTTGCAGAGACAGTGTCTCC 840
DB 781 GGAATGACTGATCCGAGCGGAGGAGAGATTTGCTTGCAGAGACAGTGTCTCC 840
QY 841 ATCCCTCCAGATGACAAACAGACGATGCTGGAGGCTGCTCTCTCTCTGATGCTG 900
DB 841 ATCCCTCCAGATGACAAACAGACGATGCTGGAGGCTGCTCTCTCTCTGATGCTG 900
QY 901 CTGGTGGCTGTGTGGGTGCTGCACTGGGATCTAATCTTGAAGGCAAGAGAGAC 960
DB 901 CTGGTGGCTGTGTGGGTGCTGCACTGGGATCTAATCTTGAAGGCAAGAGAGAC 960
QY 961 ACAGAAACGCTCTTTCTATTTCACCAATGCTTCGCCCCCTATTAAAGTCTGTGTT 1020
DB 961 ACAGAAACGCTCTTTCTATTTCACCAATGCTTCGCCCCCTATTAAAGTCTGTGTT 1020
QY 1021 TATCTCTGAGATATGTTTCCATCATCACCGTCTGTGCTTCACTGACTTTCTTCAAC 1080
DB 1021 TATCTCTGAGATATGTTTCCATCATCACCGTCTGTGCTTCACTGACTTTCTTCAAC 1080
QY 1081 TACTGAGAGATGAGTCACTCTTGAATAATGAGAAAAAGAAAAATCGCAGATGGGG 1140
DB 1081 TACTGAGAGATGAGTCACTCTTGAATAATGAGAAAAAGAAAAATCGCAGATGGGG 1140
QY 1141 CCGGTACAGTGTGACCACTCAGAAAGAGGCGAGATTAAGTGTCTTCTTCTCC 1200
DB 1141 CCGGTACAGTGTGACCACTCAGAAAGAGGCGAGATTAAGTGTCTTCTTCTCC 1200
QY 1201 AGTACGTCCTCCACCTTTGTGACAGTGTGCTGSCAATAGAGGGCAGCCAGAGAG 1260
DB 1201 AGTACGTCCTCCACCTTTGTGACAGTGTGCTGSCAATAGAGGGCAGCCAGAGAG 1260
QY 1261 AACTCTCAGGATCTGTTCCCTCTTGCTTAACTCTTTGTAGATTTGACAGCAG 1320
DB 1261 AACTCTCAGGATCTGTTCCCTCTTGCTTAACTCTTTGTAGATTTGACAGCAG 1320
QY 1321 AGCATCTGACAAATACCTGCTGTATCTTGGGGAGAGACCTCAAGGCCACTAT 1380
DB 1321 AGCATCTGACAAATACCTGCTGTATCTTGGGGAGAGACCTCAAGGCCACTAT 1380
QY 1381 AATGCCCTGAGTGTGCGCCCAATATCATCTCAGAAAGAGAGCCACAGCTTTCCACA 1440
DB 1381 AATGCCCTGAGTGTGCGCCCAATATCATCTCAGAAAGAGAGCCACAGCTTTCCACA 1440
QY 1441 GAACTTCTCAAGGCTACGAGAGATGTCAAGTGAAGAAACGCTCAAGCCCTGATAT 1500
DB 1441 GAACTTCTCAAGGCTACGAGAGATGTCAAGTGAAGAAACGCTCAAGCCCTGATAT 1500
QY 1501 AGCTGTTCACTCTTGTAGTCCACCGGGGGAATTAAGACTGTGAAGCTTCTACTTCC 1560
DB 1501 AGCTGTTCACTCTTGTAGTCCACCGGGGGAATTAAGACTGTGAAGCTTCTACTTCC 1560
QY 1561 CTTCAGTACAAATGCTGTGAGAGCTGTAATGTGTGGAGAGAGCTGTGTGAGGT 1620
DB 1561 CTTCAGTACAAATGCTGTGAGAGCTGTAATGTGTGGAGAGAGCTGTGTGAGGT 1620
QY 1621 AGTGTATGTACAACTTGCTTAAACTGGAATTTGCAAAATCACTGAGCATACAG 1680

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Db 1621 AGTGTATGTACAACTGCTTTAAAACTGGAGTTTGCAAGTCAACCTGAGCATACAG 1680
 Qy 1681 CCTGAGGAGTACATGCTGCTGATTTATGAAACACACAGTTACAGACATATATAGTG 1740
 Db 1681 CCTGAGGAGTACATGCTGCTGATTTATGAAACACACAGTTACAGACATATATAGTG 1740
 Qy 1741 GGAACCTACATTTGGATATATACCAAAAGCTGGTATATGATTTATCATCTGAGAACCCAGCT 1800
 Db 1741 GGAACCTACATTTGGATATATACCAAAAGCTGGTATATGATTTATCATCTGAGAACCCAGCT 1800
 Qy 1801 CTGGCCATGAAATATACGCACTTCCCTGTCAGGCTGCTGTCAGTGGTGGTCTGCTT 1860
 Db 1801 CTGGCCATGAAATATACGCACTTCCCTGTCAGGCTGCTGTCAGTGGTGGTCTGCTT 1860
 Qy 1861 GCACTGCCCAGTCTATGCTGACAGTACAGCTTTTGTATCATTTTATCTGTTATGA 1920
 Db 1861 GCACTGCCCAGTCTATGCTGACAGTACAGCTTTTGTATCATTTTATCTGTTATGA 1920
 Qy 1921 ATTAATCCGTTTGGGAAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963
 Db 1921 ATTAATCCGTTTGGGAAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963

RESULT 2

AAD13446 AAD13446 standard; cDNA; 2589 BP.

AC AAD13446;

DT 06-NOV-2001 (first entry)

XX Mouse interleukin-17 receptor related protein (Evi127) encoding cDNA #2.

KW Mouse; interleukin-17 receptor related protein; IL-17; chromosome 14;
 KW Evi127; retroviral integration; chromosomal mapping; mutational analysis;
 KW BXH murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy;
 KW haematopoietic cell; cancer; autoimmune disease; B8.

OS Mus sp.

XX Location/Qualifiers

PH Key 19..1511

FT CDS /*tag= d

FT /product= "Mouse Evi127 protein"

FT /transl_except= "(pos:162..163, aa:Cys-Leu)"

FT /note= "Insertion of 626 bases alters the reading

FT frame; CDS does not include stop codon"

FT /partial

XX W0200157202-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03518.

XX 04-FEB-2000; 2000US-0180374.

XX (UYAR-) UNIV ARKANSAS.

XX Shaughnessy JD;

XX MPI; 2001-496920/54.

XX P-PSDB; AAB07163.

XX New nucleic acid encoding an interleukin (IL)-17 receptor related

XX protein for use as a marker for leukemia

XX Claim 1a; Page 77-78; 87bp; English.

XX The present sequence is a cDNA encoding mouse interleukin (IL)-17

XX receptor related protein (Evi127). Mouse Evi127 gene was mapped to

XX chromosome 14. Evi127 is a common site of retroviral integration

XX in BXH murine myeloid leukaemias. Evi127 cDNA sequences are useful

CC as antisense molecules to inhibit Evi127 protein or for chromosomal
 CC mapping or mutational analysis of Evi127 protein. They are proviral
 CC integration sites associated with leukemias and monitoring this
 CC site provides a genetic tag for disease gene identification. The
 CC proteins of the invention are useful to stimulate the secretion of
 CC proinflammatory cytokines such as IL-8 and plays an important role
 CC in the developmental and/or disease processes of haematopoietic
 CC cells. Hence modulating the expression of Evi127 at the RNA or
 CC protein level is used in the treatment of diseases such as cancer
 CC or autoimmune diseases.

XX Sequence 2589 BP; 642 A; 628 C; 643 G; 676 T; 0 other;

Query Match 75.0%; Score 1472.2; DB 22; Length 2589;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 487 TTCACCTGCGCCAGGCTGCTTAAACCAAGTAATATATAAAGACGTGACGTAGGCG 546
 Db 1113 TTCACATTCGCCAGGCTGCTTAAACCAAGTAATATAAAGACGTGACGTAGGCG 1172
 Qy 547 GGAAGCCTGTGGGAGCCAGACATCACTGCTTAAAGAAAGAGAGATGGTTGAAGTG 606
 Db 1173 GGAAGCCTGTGGGAGCCAGACATCACTGCTTAAAGAAAGAGAGATGGTTGAAGTG 1232
 Qy 607 AATTTCACACCAATCCCTTGAAGACATACAGATTCTGATTCACGAGACACAGCA 666
 Db 1233 AATTTCACACCAATCCCTTGAAGACATACAGATTCTGATTCACGAGACACAGCA 1292
 Qy 667 TTGGGGTTTTCTTAAGTGTGTGAGATTAATAGTATGAGAGCCTGTATGACCATCCCGGTG 726
 Db 1293 TTGGGGTTTTCTTAAGTGTGTGAGATTAATAGTATGAGAGCCTGTATGACCATCCCGGTG 1352
 Qy 727 ACTGAGGAGATGAGTGGTGGTGTGACGTGACCCCATATTTACATACCGGCGCAT 786
 Db 1353 ACTGAGGAGATGAGTGGTGGTGTGACGTGACCCCATATTTACATACCGGCGCAT 1412
 Qy 787 GACTGCATCCGACGCGAAGGAGACATTTGCTTCTCAGAGACAAAGTCCCATCCCT 846
 Db 1413 GACTGCATCCGACGCGAAGGAGACATTTGCTTCTCAGAGACAAAGTCCCATCCCT 1472
 Qy 847 CCAGATGACACACAGCATGCTGGGAGGCTGGCTCTCTTCTGTGCTGCTGTG 906
 Db 1473 CCAGATGACACACAGCATGCTGGGAGGCTGGCTCTCTTCTGTGCTGCTGTG 1532
 Qy 907 GCTGTGTGGTGTGGTGGTGGTGTGACCTTACCTTGAAGGACAAAGGACGAG 966
 Db 1533 GCTGTGTGGTGTGGTGGTGGTGTGACCTTACCTTGAAGGACAAAGGACGAG 1592
 Qy 967 ACGTCTTTCTTATTTCCACCATGCTGCTGCTCATTTAAGTCTGTGATATCTT 1026
 Db 1593 ACGTCTTTCTTATTTCCACCATGCTGCTGCTCATTTAAGTCTGTGATATCTT 1652
 Qy 1027 TCTGAGATATGTTTCCATCACACGCTGTGTGCTTCACTGACTTCTTCAAACTACTGC 1086
 Db 1653 TCTGAGATATGTTTCCATCACACGCTGTGTGCTTCACTGACTTCTTCAAACTACTGC 1712
 Qy 1087 AGAAGTGAAGTATCTCTTGAAGAAATGCGAAGAAATGCGGAGATGGGGCCGGTA 1146
 Db 1713 AGAAGTGAAGTATCTCTTGAAGAAATGCGAAGAAATGCGGAGATGGGGCCGGTA 1772
 Qy 1147 CAGTGGCTGACACTCAGAGGAGGAGGAGTAAGTGTCTTCTTCTTCCAGTGC 1206
 Db 1773 CAGTGGCTGACACTCAGAGGAGGAGGAGTAAGTGTCTTCTTCTTCCAGTGC 1832
 Qy 1207 GTCCGACCTTTTGTGACAGTGTGCTGTGCGCAATGAGGCGAGGAGGAATCTT 1266
 Db 1833 GTCCGACCTTTTGTGACAGTGTGCTGTGCGCAATGAGGCGAGGAGGAATCTT 1892
 Qy 1267 CAGGATCTGTTCCCTTGTGACCTTTTATGATTTATGAGACGAGAGCGAT 1326
 Db 1893 CAGGATCTGTTCCCTTGTGACCTTTTATGATTTATGAGACGAGAGCGAT 1952

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Qy 1327 CTGCACAAATACCTGATGCTATCTTTGGGGAGACCTCAAGGCGACTATATATGCC 1386
    |||
Db 1953 CTGCACAAATACCTGATGCTATCTTTGGGGAGACAGACCTCAAGGCGACTATATATGCC 2012
Qy 1387 CTGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCCACAGCTTTCCACAGAACTT 1446
    |||
Db 2013 CTGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCCACAGCTTTCCACAGAACTT 2072
Qy 1447 CTGAAGGCTACGACAGCATGTAGTAAGAAAGCTCAAGGCTCCATGATAGCTGT 1506
    |||
Db 2073 CTGAAGGCTACGACAGCATGTAGTAAGAAAGCTCAAGGCTCCATGATAGCTGT 2132
Qy 1507 TCACCCCTTGTAGTCCACCGGGGAAATAGAAGACTCTGAGCCTTCTACTCTCCCTTCCA 1566
    |||
Db 2133 TCACCCCTTGTAGTCCACCGGGGAAATAGAAGACTCTGAGCCTTCTACTCTCCCTTCCA 2192
Qy 1567 GTGACAAATGCTGTGTACGACCTTGAAATGTGTGGAGAGGCTGTGTGAGTATGCT 1626
    |||
Db 2193 GTGACAAATGCTGTGTACGACCTTGAAATGTGTGGAGAGGCTGTGTGAGTATGCT 2252
Qy 1627 ATGTACAAACCTGCTTAAATAGATGATTTGCAAAAGTCAACCTGAGCATACAGCCTGAG 1686
    |||
Db 2253 ATGTACAAACCTGCTTAAATAGATGATTTGCAAAAGTCAACCTGAGCATACAGCCTGAG 2312
Qy 1687 GCTAGTCATTTGGCTGATTTATGAAGCAACACAGTTACAGACATATATGATGGAGCT 1746
    |||
Db 2313 GCTAGTCATTTGGCTGATTTATGAAGCAACACAGTTACAGACATATATGATGGAGCT 2372
Qy 1747 ACATTTGGGATATATACCAAGCTGGGTAATGATTAATCATGAGAACACAGCCTCTGGCC 1806
    |||
Db 2373 ACATTTGGGATATATACCAAGCTGGGTAATGATTAATCATGAGAACACAGCCTCTGGCC 2432
Qy 1807 ATGAAGTATATACGCACTTCCCTGTCAGGCTGTCTGTCAAGTTGGGCTCTCTTTCACATG 1866
    |||
Db 2433 ATGAAGTATATACGCACTTCCCTGTCAGGCTGTCTGTCAAGTTGGGCTCTCTTTCACATG 2492
Qy 1867 CCCATGCTATGCTGACGCTAGACCGCTTTTGTACATTTTATCTGTATATGAATATATC 1926
    |||
Db 2493 CCCATGCTATGCTGACGCTAGACCGCTTTTGTACATTTTATCTGTATATGAATATATC 2552
Qy 1927 CGTTTGGGAGCTCTCAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1963
    |||
Db 2553 CGTTTGGGAGCTCTCAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2589

RESULT 3
AADI2581
ID AADI2581 standard; cDNA, 1818 BP.
XX
AC AADI2581;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain encoding cDNA clone HP10758.
XX
KW Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antifertility; antiinflammatory; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 26..1534
FT FT /*tag= a
FT FT /product= "Human protein having hydrophobic domain"
FT FT /note= "CDS is specifically is claimed in claim 3"
FT sig_peptide 26..70
FT mat_peptide 71..1531

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FT FT /*tag= c
FT FT /product= "Mature human protein with hydrophobic domain"
PN MO200149728-A2.
PD 12-JUL-2001.
XX PF 28-DEC-2000; 2000WO-JP09359.
XX PR 06-JAN-2000; 2000JP-0000585.
XX PR 06-JAN-2000; 2000JP-0000588.
XX PR 11-JAN-2000; 2000JP-0002299.
XX PR 03-FEB-2000; 2000JP-0026862.
XX PR 03-MAR-2000; 2000JP-0058367.
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
PI Kato S, Kimura T;
XX MPI; 2001-418355/44.
DR P-PDB; AAE06586.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation.
PS Claim 4; Page 340-344; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain encoding
CC cDNA clone HP10758. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
SQ Sequence 1818 BP; 522 A; 447 C; 404 G; 445 T; 0 other;

Query Match 50.4%; Score 989.8; DB 22; Length 1818;
Best Local Similarity 77.9%; Pred. No. 6.8e-293;
Matches 1249; Conservative 0; Mismatches 337; Indels 17; Gaps 4;
Qy 6 CAGTGGCGGGGCGATGCTAGTGTGCTGATCTTGGCTGATGTGAGAGGCGCCT 65
    |||
Db 13 CAGTGGCGGGGCGATGCTAGTGTGCTGATGCTGAGCGGCGCTGTGAGAGGCGCCT 72
Qy 66 GCCTGAGAGCCGACATATTCAGTGTGCTCTGAGACAGGGCCATCTCCAGATGATGT 125
    |||
Db 73 ACCCGAGAGCCGACCGCTTCAATGAGCTCTGAAATCGGGCCATCTCCAGATGATGT 132
Qy 126 CCAACACACATCTACTCCAGAGACTTGAAGGACCTCCAGTGAACCTGCTCAAGCAAG 185
    |||
Db 133 ACAACATGATCTAATCCCGGAGACTTGAAGGACCTCCAGTGAACCTGCTCAAGCAAG 192
Qy 186 TGTGGAGAGAGAGATTTTCAATTTGATGAACATATAGCTGATATCCGGGAGAGAGCC 245
    |||
Db 193 TGTTCACACAGGAGACTATTCATTTTATGATGAATGATGAGCTGGGATCTCCGGGACAGATGC 252

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Qy	246	CAGATCCGCTGTGTTGAAGGCACCAAGATCTGCGTGAAGGCGCAAAAACAATGAATTC	305
Db	253	CAGATCCGCTGTGTTGAAGGCACCAAGATTTTGTGACGGGGAAAAGCACTTCAGTC	312
Qy	306	ATACAGCTGTGTGAGTGCACACTACAGAGGCGCTTCCAAAGCCAGACACGACTTCCG	365
Db	313	CTACAGCTGTGTGAGTGCATTTACACAGAGGCGCTTCAGACTCAGACCCAGCCCTCG	372
Qy	366	CGGCAATGGAATTCTTCCTATGTAGGCTTCCCTGTGAGCTGAGCACTCTATCTCAT	425
Db	373	TGTGAATATGCACTTTTCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAT	432
Qy	426	CAGGGCCCATPAACAATCCCAATGCTAATATGAATGAGACAGCCCTTCTTCTCTGTAA	485
Db	433	TGGGGCCCATPAATATTTCTAATGAAATATGAATGAAATGAGCCCTTCATCTGTGAA	492
Qy	486	CTTACCTCCGACGAGCTGCCCTAAACCACTGATGAATATATAAAAAGCAGTGCATGAGGC	545
Db	493	TTTCACTCTACACGAGCTGCTTACACCACTATATGAATATATAAAAAAGTGTGTCAAGCC	552
Qy	546	GGGAAGCCTGTGGGACCCAGACATCATCTGCTGTAAAAAAGAACGAGAATGTTGAAGT	605
Db	553	CGGAAGCCTGTGGGATCGAAATCACTGCTGTAAAGAAATGAGGAGACAGTGAAGT	612
Qy	606	GAATTTCAACAACATCTCCCTTGGAAACAGATACAGATTTCTATTCAAAGGACACGAC	665
Db	613	GAATTTCAACAACCTCTCCCTGGGAAACAGATACATGAGCTTTATTCMAACAGACATAT	672
Qy	666	ATTGGGGGTTTTCTAGAGTGCAGG-----AGAAATTAACGATGAGGACGTCTGTAGC	716
Db	673	CATCGGGTTTTCTAGAGTGTGTTGACCAACCAAGAAAGAACACCGAGCTTCAGTGT	732
Qy	717	CATCCCGGTGACTGAGGAGAGTGAAGGTGCGATGTTCACTGACGTGACCCCATTTTACATC	776
Db	733	GATTCAGTGACTGGGATGATGTAAGGTGCTACGGTGAAGCTGACTCATATTTTCTCAC	792
Qy	777	CTGGGGCAATGACTGCAATCCGACGCCAAGGGAACAGTTTGTCTTGTCAAGACAAATGTC	836
Db	793	TTTGAGCAGCACTGCAATCCGACATTAAGGAAACAGTTGTGCTCTGCCCAAAACAGGGGT	852
Qy	837	TCCCATCCCTCAGATGACAAACAGACGATGCTGGGAGGTGGCTGCGCTCTCTCTGGT	896
Db	853	CCCTTTCCCTCTGGATTAACAAACAAGACAGCCGGAGGCTGGCTGCTCTCTCTCTGCT	912
Qy	897	G---CTGCTGTGCTGTGTGTGGTGTGGCAGCTGGGATCTCACTTAATTGAGGCAAG	953
Db	913	GTCCTGCTGTGGCCACATGGGGTGTGTGGGAGGAGATCTATATGTGAGGACAG	972
Qy	954	AAGGAGCAAGAAAGCTCTTTCCTAATTTCCACCATGCTCTGCCCCCTATTAAAGTCTT	1013
Db	973	AAGGATCAAGAAAGCTTCTTTTCTA---CAACCACTACTGCCCCCATTAAGTCTT	1029
Qy	1014	GGTGGTTTATCCCTCTGAGATATGTTTCCATGACACCGTCTGTGCGTTACATGACTTTCT	1073
Db	1030	TGTGGTTTATCCCATCTGAATATGTTTCCATGACACAAATTTGTATCTACTGAATTTCT	1089
Qy	1074	TCAAAACTACTGACAGATGAGGTCACTCTTGAATAATGGCAGAAAAGAAAATGGCCGA	1133
Db	1090	TCAAAACCATTTGCAAGATGATGATCACTCTTGAATAATGGCAGAAAAGAAAATGACGA	1149
Qy	1134	GATGGGCGGTACAGTGGCTGACCACTCAAGAGCAAGCGGCAGATTAAGTGTCTTCT	1193
Db	1150	GATGGGTCACTGACAGTGGCTTCCACTCAAAAGAAAGGACGACCAAGTGTCTTCT	1209
Qy	1194	TCTTCCAGTGAAGTCCCGAACCCCTTGTGACATGTGCTGTGGCAAAAGTGAAGGAGCGGC	1255
Db	1210	TCTTTCATATGCTCAACAGTGTGTGCAATGTATCCTGTGGCAAGAGCAAGGAGCGATCC	1265
Qy	1254	CAGGAGAACTCTCAGAGATCTGTCCCTCTTGCGCTTTAACTCTTTTGTAGTGAATTTGAG	1313
Db	1270	CAGTGAAGAACTCTAAGACCTCTTCCCTCTTGCTTTAACTTTTGTGAGATGATTAAG	1328
Qy	1314	CAGCCAGACGATTCGACAAATATCTGTGTGTATCTTGGGGGAGCAGACCTCAAGG	1373

Db	1330	AGGCAATTCATCTGCACAAATACGTGGTCTTACTTAAAGAGATTGATACAAAAGA	1389
Qy	1374	CGACTATTAATGCCCTGAGTGTCTGCCCCCAATATCATCTCATGAAGAAGCCCAAGCTTT	1433
Db	1390	CGATTACAAATGCTCTCAGTGTCTGCCCCCAAGTACCACTCATGAAGAAGTACCACTGCTTT	1449
Qy	1434	CCACACAGAACTTCTCAAGCTTACGCGAGAGCATGTATAGTGAAGAAAAGCTCACAGCTTG	1493
Db	1450	CTGTGCAAACTTCTCCATGTCTCAAGAGAGAGGTGTGTAGAGAGAAAAGATCACAAGCTTG	1509
Qy	1494	CCATGATAGAGCTGTACCCCTTGTATGTCACCCGGGGGAA--TAGAGACTCTGAAGCTTTC	1551
Db	1510	CCAGATAGGCTGCTGCTCTTGTAGCCCAACCATGATGAAGAGCAAGACCTTAAAGGCTTC	1569
Qy	1552	CTACTCTCCCTCCAGTACAAATGCTGTGTGACGACTCTGAA	1594
Db	1570	CTATCCCAACAATTACAGGGGAAAAACGTGTATGATCTCTGAA	1612
RESULT 4			
AC	AAD28776	ID AAD28776 standard; DNA; 1841 BP.	
XX	AAD28776;		
XX	07-MAY-2002	(first entry)	
DE	Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.		
XX	Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.		
XX	Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;		
KW	cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;		
KW	autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;		
KW	infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;		
KW	cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;		
KW	eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;		
KW	epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;		
KW	leukemia; retinal neuropathy; infertility; miscarriage; inflammation;		
KW	cancer; diabetes; ds		
XX	Homo sapiens.		
XX	OS		
XX	Key	Location/Qualifiers	
XX	CDS	50..1558	
FT	FT	/*tag= a	
FT	FT	/product= "Human IL-17RB-2 protein"	
FT	FT	50..92	
FT	FT	/*tag= b	
FT	FT	93..1555	
FT	FT	/*tag= c	
FT	FT	/product= "Mature IL-17RB-2 protein"	
XX	WO200208285-A2.		
XX	31-JAN-2002.		
XX	21-JUN-2001; 2001WO-US19861.		
XX	22-JUN-2000; 2000US-213125P.		
XX	02-FEB-2001; 2001US-266159P.		
XX	16-MAR-2001; 2001US-0810384.		
XX	(AMGE-) AMGEN INC.		
XX	Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;		
XX	WPI; 2002-155217/20.		
XX	P-PSDB; AAB18127.		
XX	Nucleic acid molecules encoding Interleukin 17 (IL-17) - like		
XX	polypeptides useful in the treatment, prevention and diagnosis of		
XX	diseases e.g. cancer		

XX Disclosure; Page 230-232; 242p; English.
 XX The invention relates to nucleic acid molecules encoding Interleukin 17
 XX (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
 XX of IL-17 protein in an animal. The IL-17 protein is useful for treating,
 XX preventing or ameliorating a disease, such as immune system dysfunction
 XX (rheumatoid arthritis, osteoarthritis, inflammatory joint disease),
 XX autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
 XX disease, transplant rejection, graft vs. host disease), infections (HIV,
 XX hepatitis, bacterial), weight disorders (obesity, anorexia, cachexia,
 XX sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
 XX (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
 XX (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
 XX (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
 XX atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma
 XX leukemia); reproductive (infertility, miscarriage, endometriosis), eye
 XX (blindness, retinal neuropathy) and treatment of diseases involving
 XX inflammation. The present sequence is human Interleukin-17 receptor B-2
 XX (IL-17RB-2) DNA.

SO Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;

Query Match 50.3%; Score 988.2; DB 24; Length 1841;
 Best Local Similarity 77.9%; Pred. No. 2.1e-292;
 Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;

QY 6 CAGTGGCCGGGCGCATGTTGCTAGTGTGCTGATCTTGGCTGCATCCGCGAGAGCGCCCT 65
 DB 37 CAGTGGCCGGGCGCATGTTGCTAGTGTGCTGATCTTGGCTGCATCCGCGAGAGCGCCCT 96
 QY 66 GCCTCGAGAGCCGACTATTCAGTGTGCTGCTGAGACAGGGCCATCTTCAGAGTGTATGT 125
 DB 97 ACCCGGAGAGCCGACTATTCAGTGTGCTGCTGAGAACTGGCCCATCTTCAGAGTGTATGT 156
 QY 126 CCAACACACTCTACTCTCAGAGAGACTTGGAGACTTCAAGTGAATCTGCAAGCAAG 185
 DB 157 ACAACATGATCTATCCCGAGAGCTTGAAGGAGCTCCGAGTGAACCTTTCAACTAG 216
 QY 186 TGTGGCAGCAGAGAGTTCATTTGATGAACATTAAGCTGATCCGGGAGAGCG 245
 DB 217 TGTGGCAGCAGGAGCTATTTGATGAACATTTGATGAACATTTGATGATGCTCCGGGAGATGC 276
 QY 246 CAGCATCCGCTTGTGAAGCCACCAAGATCTGCTGATGAGGCAAAACAACTGAATTC 305
 DB 277 CAGCATCCGCTTGTGAAGCCACCAAGATTTGTGTGAAGGCAAAACAACTTCAGATC 336
 QY 306 ATACAGCTGTGATGAGTCACTACACAGAGCCCTTCAAAAGCCAGACCAAGCTTCGG 365
 DB 337 CTACAGCTGTGATGAGTCACTACACAGAGCCCTTCAAGACTCAGACCAAGCTTCGG 396
 QY 366 CGGCAATGAGCATTCCTCAATGATGAGCTCCCTGAGAGCTGAGCACTCTATCTCAT 425
 DB 397 TGTGAATGAGCATTCCTCAATGATGAGCTCCCTGAGAGCTGAGCACTCTATCTCAT 456
 QY 426 CAGCGCCCATTAACATCCCAATGATGATGAATGAGAGAGCCCTTCTTGTCTGTGA 485
 DB 457 TGGGGCCCATTAATTCCTTAATGATGAATGAGAGAGCCCTTCTTGTCTGTGA 516
 QY 486 CTTCAGCTCCGAGGCTGCTTAAACAGTAAATATTAATAAGAGTGAAGCACTGAAGC 545
 DB 517 TTTACACCTCAAGGCTGCTTAAACAGTAAATATTAATAAGAGTGAAGCACTGAAGC 576
 QY 546 GGAAGCTGTGGAAGCCACATCACTGCTTAAATAAAGAGAGATGTTGAAGT 605
 DB 577 CGAAGCTGTGGAAGCCACATCACTGCTTAAATAAAGAGAGATGTTGAAGT 636
 QY 606 GAATTCACAAACATCCCTTGAAGAGATACAGATTCAGATTCATTCAGAGGAGACGAC 665
 DB 637 GAATTCACAAACATCCCTTGAAGAGATACAGATTCAGATTCATTCAGAGGAGACGAC 696
 QY 666 ATGGGGTTTCTAGAGTCTGG-----AGATTAACATGATGAGAGCTGTGAGC 716

DB 697 CATCGGGTTTCTCAGTGTGTTGAGCCACACCAAGAAACAAACGAGCTTCAAGTGT 756
 QY 717 CATCCGGTACTGAGAGAGTGAAGTGGCGGTGTTGAGTCACTGACCCCATATTATCATAC 776
 DB 757 GATTCAGTACCTGGGGATAGTGAAGTGTCTAGCGTGAAGTCACTGACCTCATATTTCTCAC 816
 QY 777 CTGGGCAATGACTGATCCGACGCGAAGGACAGTTGTCTTGTCTCAAGACAAAGTGC 836
 DB 817 TTGTGACAGAGCTGATCCGACATTAAGGAACAGTTGTGTCTGTGCCCAACAGGCGT 876
 QY 837 TCCATCCCTCCAGATGACACAGAGCATGCTGGAGGCTGCTGCTCTCTGTCT 896
 DB 877 CCTTTCTCTGGAATAACAAAGAGAGCGGAGGCTGCTCTCTCTGTCT 936
 QY 897 G---CTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 953
 DB 937 GTCTCTGCTGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 996
 QY 954 AAGAGCAGAGAGAGCTCTTTCTTATTTTCAACATGCTCTGCTGCTGCTTAAAGTCT 1013
 DB 997 AAGATCAAGAGAGCTCTTTCTTATTTTCAACATGCTCTGCTGCTGCTTAAAGTCT 1053
 QY 1014 GGTGTTTATCTTCTGAGATATGTTTCCATCATCACACCGTCTGCTGCTGCTGCTGCT 1073
 DB 1054 TGTGTTTATCCATCTGAATATGTTTCCATCATCACCAATTTTCTTCACTGAATTTCT 1113
 QY 1074 TCAAACTACTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1133
 DB 1114 TCAAACTACTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
 QY 1134 GATGGGCGGATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1193
 DB 1174 GATGGGCGGATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
 QY 1194 TCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
 DB 1234 TCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
 QY 1254 CAGGGAAGTCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313
 DB 1294 CAGTGAAGTCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1353
 QY 1314 CAGCAGAGCATCTGACCAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373
 DB 1354 AAGCAGATTCATCTGACCAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1413
 QY 1374 CGACTTATATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433
 DB 1414 CGATTAATGCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473
 QY 1434 CCAACAGAACTTCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1493
 DB 1474 CTGTGCAAACTTCTCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1533
 QY 1494 CCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
 DB 1534 CCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1593
 QY 1552 CTACTCTCCCTTCAAGTGAATGCTGTGTGAGCACTGTGA 1594
 DB 1594 CTATCCCACTTCAAGGAAACAGTGTGATGCTGTGA 1636

RESULT 5
 ABA03200
 ID ABA03200 standard; cDNA; 1841 BP.
 XX
 AC ABA03200;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Human IL-17 receptor like protein #1 coding sequence.
 XX

Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic; antipsoriatic; antimicrobial; anorectic; nocotropic; neuroprotective; antiaschemic; antiallergic; dermatological; cytoskeletal; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye; tumour; ss.

Homosapiens.

Key Location/Qualifiers
50..1558
/tag= a
/product= "Human IL-17 receptor-like protein #1"

W0200168705-A2.

20-SEP-2001.

16-MAR-2001; 2001WO-US08688.

16-MAR-2000; 2000US-189923P.
12-MAY-2000; 2000US-204208P.
27-NOV-2000; 2000US-0722232.
02-FEB-2001; 2001US-266159P.

(AMGE-) AMGEN INC.

Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ.
WPI: 2002-055100/07.
P-PSDB; AAM47456.

Three human nucleic acids encoding interleukin 17 (IL-17) receptor like polypeptides, useful for treating, diagnosing, ameliorating or preventing immune system disorders (e.g. psoriatic arthritis) and infections (e.g. viral infections)

Claim 1; Fig 1; 239pp; English.

The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. ischaemia), eye disorders, reproductive disorders, tumours and inflammation.

Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;

Query Match 50.3%; Score 988.2; DB 24; Length 1841;
Best Local Similarity 77.9%; Pred. No. 2.1e-292;
Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;

6 CAGTGGCCGGCCATGTTGCTAGTGTGCTGATCTTGGTCGATGTCGAGAGAGCCCT 65
Db 37 CAGTGGCCGGCGATGTCCTGCTGCTAGCCCTGGCGGCTGTGAGAGAGCCCT 96

66 GCGTCGAGAGCCGACATATTCAGTGTGGCTCTGAGACAGGGCCATCTCGAGTGTGT 125
Db 97 ACCCGAGAGCCGACCTGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGATGTGATGCT 156

126 CCAACACACACTCTCTCAGAGAGACTTGAAGGACCTCCAACTGGAACCTGTCAAGACAAG 185
Db 157 ACAACATGATTAATCCCGGAGACTTGAAGGACCTCCAGTAGAACTGTAAACAATG 216

166 TGTGTCGAGAGAGAGATTTTCAATTTTGAATGAACATTAAGTGTGATCTCCGGGACAGCC 245
Db 217 TGTTCGAACAGGGGACTATTAATTTTGAATGAATGAATGAATGCTGGGTAATCCGGGACAGATGC 276

246 CAGCATCCGCTTGTGTAAGGCCACCAAGATCTGCGTAGGTGGCAAAAACAATGAATTC 305
Db 277 CAGCATCCGCTTGTGTAAGGCCACCAAGATTTGTGAGAGGGGAAAAGACATTCAGTC 336

306 ATACAGCTGTGTAGGTGCACTACACAGAGGCTTCCAAAGCCAGACCAAGCTTCCGG 365
Db 337 CTACAGCTGTGTAGGTGCAATTAACAGAGGCTTCCAGACTCAGACCAAGCCCTCTGG 396

366 CGGCAATGAGACATCTCTATGTAGGCTTCCCTGTGAGCTGAGACCTCATCTCAT 425
Db 397 TGTAAATGAGACATTTTCTTCAATAGGCTTCCCTGTGAGCTGAGACAGTCAATTTCA 456

426 CAGCGCCATAACATCCCAATGCTAATATGATGAGAGACAGCCCTTCTTGTCTGAA 485
Db 457 TGGGGCCATATATTTCTTAATGCAATATGATGATGAATGAGTGCCCTTCATGTCTGAA 516

486 CTTCACCTTCCAGAGGCTGCTTAACCAAGTAAATGAATTAATAAGCAAGTGAAGGC 545
Db 517 TTTCACTTCAACAGGCTGCTTGAACCAATTAATGAATTAATAAAGTGTCAAGGC 576

546 GGGAGCCGTGTGGGACCCAGACATCATGCTGTAAATAAAGAAAGAGAGTGTGAAGT 605
Db 577 CGAAGCTGTGGATCCGAACATCATGCTGTGTAAGAAATGAGAGACAGTAGAGT 636

606 GAATTTCAACAACCAATCCCTTGGAAACAGATATCAATTCATTCACAGGACACAGAC 665
Db 637 GAATTTCAACAACCAATCCCTTGGAAACAGATATGAGTGTCTTATTCACACAGACTAT 696

666 ATTTGGGTTTCTTGAAGTCTGG-----AGATAAATCTGATGAGAGCGTCTGTAC 716
Db 697 CATCGGTTTCTTCAAGTGTGTGAGACCAACCAAGAAACAAAGCGGAGTTCAGTGT 756

717 CATCCCGTGAATGAGAGAGTGAAGTGGGTGTGACGTGACGACCCATTTATCATAC 776
Db 757 GATTCAGAGTGTGGAGATGAGAGGTGTACAGGTGACGTGACGTCCATTTTCTTAC 816

777 CTGGCAATGACTGATCCGACGAGAGGACAGTGTGCTTGTCTGAGACAAAGTGC 836
Db 817 TTGTGGCAGCAGCTGATCCGACATTAAGAAACAGTGTGCTCTGCCCAACAGAGCT 876

837 TCCCATCCCTCCAGATGACACACAGACGATGCTGGAGGCTGGCTCTTCTTCTGTGT 896
Db 877 CCCTTCCCTCTGATTAACAAACAAAGCAAGCCGGAGGCTGGCTCTTCTTCTGTGT 936

897 G---CTGCTGT 953
Db 937 GTCTGT 996

954 AAGAGCAGAAAGCTCTCTTCTTATTTCCACATGCTCTGCCCTCATTAAGGTCT 1013
Db 997 AAGATCAAGAAAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1053

1014 GGTGTTTATCTTGTGATATGTTTCCATGACACCGTGTGCTTCACTGACTTCT 1073
Db 1054 TGTGTTTATCCATCTGAATAATGTTTCCATGACACCAATTTGTACTTCACTGAATTTCT 1113

1074 TCAAAATCTACGCAAAAGTGTGATCTTGAATAAATGTGCAAAAATATGCGCA 1133
Db 1114 TCAAAACATGTGCAAAAGTGTGATCTTGAATAAATGTGCAAAAATATGCGCA 1173

1134 GATGGGCGGTAAGTGTGTGACACTCAGAAAGAGGAGAGTAAGTGTGTCT 1193
Db 1174 GATGGGTCAAGT 1233

1194 TCTTCCAGTGAAGTCCGACCTTGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1253
Db 1234 TCTTCCATGATGTCACAGAGT 1293

1254 CAGGAGAACTTCAGATGT 1313
Db 1294 CAGTGAAGAACTTCAGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1353

Oy	964	AAGAGCTCTTCTTCTATTTTCCACAGAGCTCTCTCCCTCATTAAGTCTGGTGTAT	1023
Oy	964	AAGAGCTCTTCTTCTATTTTCCACAGAGCTCTCTCCCTCATTAAGTCTGGTGTAT	1023
Db	961	AAGACTTCCTTTTCTA---CCACCACTACTCTGCCCCCATTTAAGTCTTGTGGTTAC	1017
Oy	1024	CTTCTGAGATATGTTTTCATCAACACCGCTGTGCGTTCACTGACTCTTCTTCAAAATCAC	1083
Db	1018	CCATCTGAAATATATGTTTCCATACACACATTTGTTACTTCACTGAATTTCTTCAAAACAT	1077
Oy	1084	TGCGAAGTAGGTCATCTCTTGAAAAATGGCAGAAAAAAGAAATGGCCGAGATGGGGCCG	1143
Db	1078	TGCGAAGTAGGTCATCTCTTGAAAAATGGCAGAAAAAAGAAATGACAGATGGGTCCA	1137
Oy	1144	GTCAGAGGCGTCACACTCTAGAAAGCAAGCGGGCAGATTAAGTGTCTCTCTTCTCCAGT	1203
Db	1138	GTCAGATGGCTTGTGCCACTCAAAAGAAAGCAGACGACAAAGTGTCTTCTCTTTCAT	1197
Oy	1204	GAGCTCCCGACCCCTTGTGTGACAGTGCCTGTGGCCACATAGAGGGCAGCGCCAGAGAAAC	1263
Db	1198	GAGCTCAACAGTGTGTGTGATGTTGATCCTGTGGCAAGAGGAGGAGTCCAGTGAAGAC	1257
Oy	1264	TCTCAGATCTGTTCCTCTTGCCTTTAACCTCTTTTGTATGATTTTACAGACGCAAGC	1323
Db	1258	TCTCAAGACCTCTTCCCCCTTGGCTTTAACCTTTTCTGCAGTGAATCAAGAACAGATT	1317
Oy	1334	CATCTGCACAAATTCCTGTGTGTCTATCTTTGGGGGAGCAGACCTCAAAAGCGACTATAT	1383
Db	1318	CATCTGCACAAATTCCTGTGTGTCTATCTTTGAGAGATTGATTAACAAAGACATTAACAT	1377
Oy	1384	GCCCTGAGTGTCTGCCCCCAATATCATCTCATAGAGAGCCACAGCTTTCACACAGAA	1443
Db	1378	GCTCTCAGTGTCTGCCCCCAAGTACCACTTCATAGAGATGCCACTGTCTTCTGTGCAGAA	1437
Oy	1444	CTTCTCAAGGTCACGACAGACATGTCAGTGAAGAAAACGCTCAAGACCTGCCATGATAGC	1503
Db	1438	CTTCTCCATGTCAAGCAGCAGAGGTGTACGACAGAAAAAAGATCAACAGCTGCCACGATGCG	1497
Oy	1504	TGTTCAACCTCTTGTATGTCCACCCGGGGGAA--TGAGACTCTGAAGCTTCTCTATCTTCCC	1561
Db	1498	TGCTGCTCTCTGTAGCCCAACCCATAGAAAGCAAGAACCTTTAAAGCTTCTCTATCCACCC	1557
Oy	1562	TTCCAGTGACAAATGCTGTGTGACGACTCGAA	1594
Db	1558	AATTACAGGGAAAAAACGTGTGATGATCTGAA	1590
RESULT 7			
AAH99008			
ID	AAH99008 standard; cDNA; 2161 BP.		
XX	AAH99008;		
AC	12-OCT-2001 (first entry)		
XX			
DT			
XX			
DE	Human EST-derived coding sequence SEQ ID NO: 865.		
XX			
KW	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;		
KW	tomato; monkey; dog; sea urchin; expressed sequence tag; EST;		
KW	diagnostics; forensic test; gene mapping; genetic disorder;		
KW	biodiversity; gene therapy; nutrition; ss.		
OS	Homo sapiens.		
XX			
PN	WO200154477-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	25-JAN-2001; 2001WO-US02687.		
XX			
PR	25-JAN-2000; 2000US-0491404.		
PR	17-JUL-2000; 2000US-0617746.		
PR	03-AUG-2000; 2000US-0631451.		
PR	15-SEP-2000; 2000US-0663870.		

PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX	Cao Y, Drmanac RA, Zhang J, Werltman T;
XX	WPI; 2001-476164/51.
DR	P-PSDB; AAM24349.
XX	
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising
XX	antibodies and research use -
XX	
PS	Claim 1; Page 707; 1275bp; English.
XX	
CC	The present invention provides the protein and coding sequences of novel
CC	proteins from a variety of organisms, including human, dog, cat, horse,
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC	from the organism of interest. They can be used in diagnostics,
CC	forensics, gene mapping, identification of mutations, to assess
CC	biodiversity and for nutritional purposes. The present sequence is a cDNA
CC	of the invention.
SQ	Sequence 2161 BP; 639 A; 516 C; 446 G; 560 T; 0 other;
	Query Match 50.0%; Score 982.4; DB 22; Length 2161;
	Matches Local Similarity 77.9%; Pred. No. 1,4e+280;
	MATCHES 1241; Conservative 0; Mismatches 336; Indels 17; Gaps 4;
OY	15 GGCACATGTTGGCTAGTGTGTCATCTTGCGCATCGTCAGAGACGCCCTGCTCGAGA 74
Dd	4 GGCAATGTCGTGCTGCTGCTGAAGCCTGCGCGCTGTCAGAGAGCGGCTAACCCGAGA 63
OY	75 GCCGACTATTGACGTGTGCTCTGAGACAGGGCCATCTTCAGAGTGGATGTCCAACAC 134
Dd	64 GCCGACCGTTCATATGTGCTCTGAACCTGGGACCATCTTCAGAGTGGATGTCCAACATGA 123
OY	135 ACTCACTCCAGAGACCTTGAAGACCTCCAACTGGAATCTGTCGAAGACAATGTGGCAGC 194
Dd	124 TCTATATCCCGGAGACTTGAAGGACCTTCGAGTAGAATCTGTTCACATTAATGTGGCAC 183
OY	195 AGAGAGATTTTTCAATTTTGTGATAACATTAAGCTGTATCTCCGGGACAGCGCAGCATCCG 254
Dd	184 AGGGGACATATTCATTTTGTGATGATGATGAGTGGTACTCCGGGCAAGATGCAAGATCCG 243
OY	255 CTGTGTGAAGGCCAACAGATCTGCTGAGTGGCAAAAACAATGAATTCAATCAAGCTG 314
Dd	244 CTGTGTGAAGGCCAACAGATTTGTGTGACGGGCAAAAAGCAATCTTCAGTCTCAAGCTG 303
OY	315 TTGTGAGTGCATACACACAGAGGCTTCCAAAGCCACACAGACTCTCCGGCGGCAATG 374
Dd	304 TTGTGAGTGCATATTAACACAGAGGCTTCCAGACTCAAGCCAGACCTCTGTGTGTAATG 363
OY	375 GACATTTCTCCATGATGAGGCTCCCGTGGAGCTGAGCATCTCATCTCATCAGAGGCCA 434
Dd	364 GACATTTTCTCAATTCGGCTTCCCTGTGAGACTGAACAGATCTAATTTTCATTTGGGACCA 423
OY	435 TAACATCCCCCATGCTAATATGAATGAAGACAGGCTTCTTTGTGTGAACTTCACTTC 494
Dd	424 TAATTTCTTAATGCAAAATATGAATGAAGATGGGCTTCCATGTCGTGAAATTCACCTC 483
OY	495 GCCAGGCTGCTTAAACACAGATATGAATAATATAAAAAGCAGTGCACCTAGGCGGAGGCT 554
Dd	484 ACCAGGCTGCTTAAACACATTAATGAATAATAAAAAAGTGTCAAGGGCGGAGGCT 543
OY	555 GTGGAGCCCAACATCACTGCTGTAAAAAAGAGAGAGATGGTGAATGAATTTTAC 614
Dd	544 GTGGAGTCCAAATCACTGCTTTGTAAGAGAAATGAGAGACAGTAAATGAATTTTAC 603
OY	615 AACCAATCCCCTTGAAGAACAGATACAGATTTCTATTCAAACGGGACAGCAATTTGGGTT 674
Dd	604 AAACACTCCCTTGGGAAACAGATATAGGCTTTATCAACACAGACACTATCATTCGGGTT 663
OY	675 TTCTAGAGTGTGG-----AGAAATAACTGATGAGACGTCCTGAACCATCCGGT 725

Db	664	TTCTCAGGTGTTTGAGCCACACCGAAGAAACAAACGCGAGCTTCACTGGTGTTCAGT	723
Qy	726	GACTGAGGAGATGAAAGTGCAGGTGTTACGCTGACCCCATATTTACATACCTGCGGCAA	785
Db	724	GACTGGGGATAGTGAAGGTGCTACCGGTGACGCTACTCATATTTTCTTACTTGTGCGAG	783
Qy	786	TGATCTGCATCCGACGCGAAGGACAGTTGTGCTTTGCTCAGAAGCAAGTGCTCCCATCC	845
Db	784	CGACTGCATCCGACATPAAAGAAACAGTTGTGCTCTGCGCCAAACAGCGCTCCCTTTCCC	843
Qy	846	TCAGATGACAAACAGACGATGCTGGGAGGCTGGCTGCTCTCTTCCCTGGNG--CTGCT	902
Db	844	TTCTGGATTACAAACAAAGCAAGCGGAGGCTGGCTGCTCTCTCTCTGCTGTCTGCT	903
Qy	903	GGTGGCTGTGTGGGTGTGTCAGCTGGATCTACTTAATTGAGCGACAGAAAGAGACAC	962
Db	904	GGTGGCCACATGGGTGTGTGTGGAGGAGCTATCTATATGTGGAGGACAGAAAGGATCAA	963
Qy	963	GAAAGAGTCTCTTCTCTATTTTCCACATGCTCTGCGCCCTCATTAAGTCTGGTGTTTA	1022
Db	964	GAAAGATTTCTTTTCTCA--CAACACACATACGCCCCCATTAAGGTTTGTGGTTTA	1020
Qy	1023	TCCTTCTGAGATATGTTTTCATACACCGTGTGCGCTTCACTGACCTTCTTCAAACTA	1082
Db	1021	CCCATCTGAATATGTTTTCATACACAAATTTGTACTTCACTGAATTTCTTCAAAACA	1080
Qy	1083	CTGCAGAAAGTAGATCATCTCTTGAATAATGGACAAATAACGACGATGGGACC	1142
Db	1081	TTTCAGAAAGTAGATCATCTCTTGAATAATGGACAAATAATAGCAGATGGGTCC	1140
Qy	1143	GGTACAGTGGCTACCACTGAAAGCAAGGCGACAGATTAAGTGTCTTCTTCTTCCAG	1202
Db	1141	AGTGCAGTGGCTTGCACCTCAAAAGAAAGGACGACGACAAAGTGTCTTCTTCTTCCAA	1200
Qy	1203	TGACGTCCCGACCTTTTGTACAGTGTCTGTGGCACAAATGAGGGACGCGCAAGGAGAA	1262
Db	1201	TGACGTCCACAGTGTGTGCGATGTGTACTGTGGCAGAGGAGGACGTCCAGTGAAGAA	1260
Qy	1263	CTCTCAGATCTGTCCCTCTTGAACCTCTTTTGTATGATTTACGACGCCAGAC	1322
Db	1261	CTCTCAAGACCTCTTCCCTTGTCCCTTTAACCTTTTCTGACATGATCTTAAGAACGAT	1320
Qy	1323	GCATCTGCACAAATTAACCTGTGTCTATCTTGGGGGACGACCTCAAGGCGACTATTA	1382
Db	1321	TCATCTGCACAAATTAAGTGTGTGTACTTTTAAAGAGATTTGAATACAAACCATTTACA	1380
Qy	1383	TGCGCTGAGGTGTGCCCCCAATATATCTCATGAAAGGACGCCAGCTTCCACACAGA	1442
Db	1381	TGCTTCAAGTGTGCCCCCAAGTACACCTCATGAAGAGATGCCATGTCTTCTGTGAGA	1440
Qy	1443	ACTTCTCAAGGCTTACCGACAGCATGTCTCATGAAAGAAACGCTCAAGCCTGCATGATAG	1502
Db	1441	ACTTCTCCATGTCAAGCGAGAGGTGTCTACGAGAGAAAGATTCACAGCCTGCCACGATGG	1500
Qy	1503	CTGTTCACCTTGTAGTCCACCCGGGAGAA--TAGAGACTCTGAAGCTTCTACTCTCTCC	1560
Db	1501	CTGTCTCTCTTGTGTAGCCCAACCATGATGAGAAAGAGACCTTAAGGCTTCTATCCAC	1560
Qy	1561	CTTCCAGTACAAATGCTGTGTATGACACTGTGAA	1594
Db	1561	CAATTACAGGAGAAAAACGTGTATGATCTGTGAA	1594
RESULT 8			
AAD13443			
ID	AAD13443 standard, cDNA, 1827 BP.		
XX	AAD13443;		
AC			
XX	06-NOV-2001 (first entry)		
DT			
XX	Human interleukin-17 receptor related protein [Evi27] encoding cDNA #1		

XX	Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21; EVI27; retroviral integration; chromosomal mapping; mutational analysis; BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy; haematopoietic cell; cancer; autoimmune disease; ss
XX	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	CDS
XX	6..1514
XX	/tag= a
XX	/product= "Human EVI27 protein"
XX	sig_peptide
XX	6..44
XX	/tag= b
XX	45..1511
XX	/tag= c
XX	/product= "Human mature EVI27 protein"
XX	mat_peptide
XX	WO200157202-A2.
XX	09-AUG-2001.
XX	02-FEB-2001; 2001WO-US03518.
XX	04-FEB-2000; 2000US-0180374.
XX	(UYAR-) UNIV ARKANSAS.
XX	Shaughnessy JD;
XX	WPI: 2001-496920/54.
XX	P-PSDB: AAE07160.
XX	New nucleic acids encoding an interleukin (IL)-17 receptor related protein for use as a marker for leukemia
XX	Claim 1a; Page 74-75; 87pp; English.
XX	The present sequence is a cDNA encoding human interleukin (IL)-17 receptor related protein (EVI27). Human EVI27 gene was mapped to chromosome 3p21. EVI27 is a common site of retroviral integration in BXH2 murine myeloid leukaemias. EVI27 cDNA sequences are useful as antisense molecules to inhibit EVI27 protein or for chromosomal mapping or mutational analysis of EVI27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proteins of the invention are useful to stimulate the secretion of proinflammatory cytokines such as IL-8 and plays an important role in the developmental and/or disease processes of haematopoietic cells. Hence modulating the expression of EVI27 at the RNA or protein level is used in the treatment of diseases such as cancer or autoimmune diseases.
XX	Sequence 1827 BP; 547 A; 438 C; 397 G; 445 T; 0 other;
XX	Query Match 50.0%; Score 980.8; DB 22; Length 1827;
XX	Best Local Similarity 77.8%; Pred. No. 4e-290;
XX	Matches 1240; Conservative 0; Mismatches 337; Indels 17; Gaps
XX	15 GGGCAGTGTGCTAGTGGCTGATCTTGGCTGCATCGTCGACAGAGCCGCTCGGAGA 74
XX	2 GGGCAGTGTGCTGCTGATGATAGCTGGCCGCGCTGTGCAGAGCCGCTGACGAGA 61
XX	75 GCCGACTATTCAGTGTGGCTGAGACAGAGGCGCATCTCCAGATGGATGCTCAACAC 134
XX	62 GCCGACCGTTCATGTGCTGGAACCTGGGCACTCCAGATGGATGCTCAACATGA 121
XX	135 ACTCACTCCAGAGACTTGAAGGACCTCCAACTGCAAGACAGTGTGGAC 194
XX	122 TCTAATCCCCGAGACTTGAAGGACCTCCGAGTAGAACCTGTTACCACTAAGTTGCAAC 181
XX	195 AGAGAGTTTCAATTGATGATGAACATAAGCTGGAATCTCGGGGAGACGCCAGATCCG 254

D	182	AGGGGACATTAATCAATTTTGGATGAACTGGATGACTCCGGGACGAGATGCCAGATCCG	241
O	255	CTTGTTGAAGGCCCAACAGATCTGCGTGAAGTGGCAAAAACACATGAAATTCATACACTG	314
D	242	CTTGTTGAAGGCCCAACAGATTTGTGTGACGGGCAAAAGCAATTCACATGCTTACAGCTG	301
O	315	TGTGAGGGCAACTACACAGAGGCTTCCAAACCCAGACACAGCTTCCTCGGGGGGAATG	374
D	302	TGTGAGGGCAATTAACACAGAGGCTTCCAGACTCAGACCCAGACCTCTGGTGGTAAATG	361
O	375	GACATTCCTCATGTAGAGCTTCCCTGTGAGCTGAGACACTCTCTATCTCATCAGCGCCA	434
D	362	GACATTTTCTCATATCGGCTTCCCTGTGAGCTGAAACACAGCTATTTATTTGGGGCCCA	421
O	435	TAAACATCCCAATCTAATATGAATGAGACAGACCCCTTCTTGTCTGTAACCTCACTC	494
D	422	TAAATATCTTAATGCAATATATGAATGAAATGAGCCCTTCATATCTGTGAATTCACCTC	481
O	495	GCCAGGCTGCTAAACCAAGTAATGAATTTAAAAAGCACTGCACTGAGGCGGAAAGCT	554
D	482	ACCAAGGCTGCTTAACCAACATATGAATTTAAAAAAAGTGTGTCAAGGCGGAAGCT	541
O	555	GTGGGACCCACACATCACTGCTGTGTAATAAAGACGAAAGATGAGTGAATTTAC	614
D	542	GTGGAGTCCAAACTCACTGCTGTGTAATAAAGATGAGAGACATATGAATTAACCTTCA	601
O	615	AACCAATCCCTTGGAAACAGATACAGATTCATTCATTCACGGGACACACATTTGGGGTT	674
D	602	AACCACTCCCTGGGAAACAGATATCATGCTCTTATTCAAACAGACATATATCGGGTT	661
O	675	TTCTAGAGTGTGG-----AGAAATACTGATGAGAGCTCTGTAGCCATCCGGT	725
D	662	TTCTCAAGTGTGTAAGCACACACAGAAAGAAAGCAAGCAGCTTCAGTGTGATTCACAT	721
O	726	GACTGAGAGAGTGAAGGTGCGGGGTGACGTACGACCCCATATTTAATACCTGGAGCA	785
D	722	GACTGGGATATGTAAAGGTCTACGGGTGACGTGACTCAATTTTCTTACTTTGGGAG	781
O	786	TGACTGATCCGACGCGAAGGAGCAGTTGTGCTTTGCTCAGAGACAAAGTCTCCATCC	845
D	782	CGATGCGATCCGACATTAAGGAACAAGTTGTGCTCTGCCAACAAGGGTCCCTTTCC	841
O	846	TCCAATGACACACAGACGCACTGCTGGGAGCTGGCTGCTCTTCTCTGGTG--CTGCT	902
D	842	TCTGGAATPACAAACAAAGCAAGCGGGAGGCTGGCTGCTCTCTCTCTCTCTCTCT	901
O	903	GGTGGCTGTGTGGGTGTGGCACTGGGATCTTACTTAACTTGAAGGACGAAGAAGAC	962
D	902	GGTGGCCACATGGGTGTGGGTGGGAGGATCTTCTTAAATGTGAAGGACGAAGAAGATCA	961
O	963	GAAAGCTCTTTCTTATTTTCCACAGTCTGCGCCCTCATTTAAGGTCTGTGGTGTTA	1022
D	962	GAAAGCTTTCTTTCTTA---CAACACACTACTGCCCCCATTTAAGTCTTGTGTGTTA	1018
O	1023	TCCTTGTGAATATGTTTTCATCAACACCGTCTGTGCTTCACTGACTTTTCAAACTA	1082
D	1019	CCCATCTGAATAATGTTTTCATCAACAAATTTGTATCTTCACTGAATTTCTTCAAAACA	1078
O	1083	CTGACAGAAATGAGGTCACTCTTGTAAAAATGCGAAGAAAAATGCGGAGATGGGGC	1142
D	1079	TTTGACAGAAATGAGGTCACTCTTGAAGATGCGAAGAAAAATATGACGAGATGGGTCC	1138
O	1143	GGTACAGTGGCTGACACTCAGAAAGCAAGGGGAGATTAAGTGTCTTCTCTTCCAG	1202
D	1139	AGTGCAGTGGCTTGCACCTCAAAAAGAGCAGACGAACAAAGTGTCTTCTTCTTTCCAA	1198
O	1203	TGACGTCCCAACCTTTTGTGACAGTGTCTGTGGCCAATATGAGGAGCGGCCAGGAGAA	1262
D	1199	TGAGGTCAACAGTGTGTGCGATGTACTGTGTGCAAGAGGAGGAGGACATCCAGTGA	1258
O	1263	CTTCTCAGAGTCTGTCCCTCTGTGCTTTAACTCTTTTGTATGATTTAGACAGCCAGAC	1322
D	1259	CTTCTCAGAGCTCTTCTTCCCTCTGTGCTTTAACTTTTCTGAGTATCTTAAAGAGCAAT	1318

Oy 1323 GCATCTSCACAAATTAACCTGGTGGTCTATCTTTGGGGAGACAGCTCAAGCGCACTATA 1382
 Db 1319 TCACTTCACAAATTAACGTGGTGGTCTACTTTGAGAGATGATACAAAAGACGATTACAA 1378
 Oy 1383 TGCCCTGAGTGTGCGCCCAATATCATCTCATGGAAGACGCACAGCTTTCCACACAGA 1442
 Db 1379 TGCTCTCAGAGTGTGGCCCAAGTACCACTTCATGGAAGATGCACTGCTTCTGTGACAGA 1488
 Oy 1443 ACTTCTCAAGGCTACGACAGAGCATGTCACTGAAGAAAGGCTCACAGGCTGCTCATGTATAG 1502
 Db 1439 ACTTCTTCATGTCAAGCAGCAGAGTGTCACAGAGAAAAGATCACAGGCTTCCACAGATGG 1498
 Oy 1503 CTGTTCACCCCTTGAAGTCCACCCGGGGGAA--TAGAGACTGGAAGCCTTCTACTCTCC 1560
 Db 1499 CTGTGCTCTCTTTAAGCCACCCATAGAGAGCAAGACCTTTAAAGGCTTCTTATCCAC 1558
 Oy 1561 CTTCGACGACGAATGCTGTGTGAGACAGCTCTGAA 1534
 Db 1559 CAATTACAGGAGAAAAAGCTGTGATGATATCTTAAA 1592

RESULT 9	
AAA75772	
ID AAA75772	standard; cDNA; 1918 BP.
XX	
AC	
XX	
XX	
XX	AAA75772;
DT	22-JAN-2001 (first entry)
DE	cDNA encoding a human interleukin 17 receptor-like protein variant.
XX	
KW	Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
KW	cellular activation; haemostasis; angiogenesis; tumour metastasis;
KW	cellular migration; ovulation or neurogenesis; arthritis;
KW	autoimmune disorder; systemic lupus erythematosus; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	CDS 111..1412
FT	/tag= a
FT	/product= "interleukin 17-receptor-like protein variant"
XX	
PN	WO200055204-A1.
XX	
PD	21-SEP-2000.
XX	
PF	06-MAR-2000; 2000MO-US05759.
XX	
PR	16-MAR-1999; 99US-0268311.
XX	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
XX	
P1	Shi Y, Ruben SM;
XX	
DR	WPI: 2000-647065/62.
DR	P-PSDB; AAB18754.
XX	
XX	
PT	Novel gene encoding a polypeptide of the interleukin-17 receptor
PT	family, and an antagonist and agonist of the polypeptide, useful for
PT	treating, diagnosing, detecting and/or preventing immune system related
PT	disorders
XX	
PS	Disclosure; Page 237-239; 247pp; English.
XX	
CC	The present sequence encodes a human interleukin 17-receptor-like protein
CC	(IL17RLP) variant. The IL17RLP polypeptide is useful for screening for
CC	agonists and antagonists. These antagonists and agonists are useful for
CC	treating, diagnosing, detecting and/or preventing disorders related to
CC	cellular activation, haemostasis, angiogenesis, tumour metastasis,
CC	cellular migration, ovulation or neurogenesis, such as osteoporosis,
CC	arthritis and autoimmune disorders e.g. systemic lupus erythematosus.
CC	

XX Sequence 1918 BP; 560 A; 469 C; 426 G; 461 T; 2 other;
 SQ Query Match 49.5%; Score 970.8; DB 21; Length 1918;
 Best Local Similarity 77.8%; Pred. No. 4.8e-287;
 Matches 1241; Conservative 0; Mismatches 337; Indels 18; Gaps 5;

13 CGGGCCATGTTGCTAGTGTGCTGATCTTGGCTTCATCGTGCAGAGAGCGCCCTCGA 72
 105 CGAGCGATGCTCGTGTGCTTAAGCTGGCCGGCTGTCAAGAGCGCCGTACCCCGA 164
 73 GAGCGCATATTCAGTGTGCTGAGACAGAGGCAATCTCCAGAGTGAATGCTCAAC 132
 165 GAGCGGACCTTCATGTGTGCTGAAACTGGGCAATCTCCAGAGTGAATGCTCAAC 224
 133 ACATCTACTCAGAGAGCTTGAGGAGACCTCCAGTGGAACTCCGCAAGACAGAGTGGCA 192
 225 GATCTAATCCCGAGACTTGAGGAGACCTCCAGTGAACCTGTTACACATAGTGTGCA 284
 193 GCAGAGAGATTTCAATTTTGATGACATAGCTGATCTCCGGGAGAGCGCCAGATC 252
 285 ACAGGGGACTTTCATTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 344
 253 CGCTTTGTAAGGCGCAAGATCTGCTGATGATGATGATGATGATGATGATGATGATG 312
 345 CGCTTTGTAAGGCGCAAGATTTGTGTGACGGGCAAAAGCAATTCAGTCTTACAGC 404
 313 TGTGTGAGTGAACCTACAGAGAGCGCTCCAAAGCGAGACCAAGCTTCCGGGGGAAA 372
 405 TGTGTGAGTGAACCTACAGAGAGCGCTCCAAAGCGAGACCAAGCTTCCGGGGGAAA 464
 373 TGAACATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
 465 TGAACATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 524
 433 CATTAATCTCCCAATGCTTAATATGATGATGATGATGATGATGATGATGATGATGAT 492
 525 CATTAATCTCCCAATGCTTAATATGATGATGATGATGATGATGATGATGATGATGAT 584
 493 TCGCAGAGTGCCTTAACCAAGTAAATATTAAGAAAGCACTGAGGGGGGAGG 552
 585 TCACAGAGTGCCTTAACCAAGTAAATATTAAGAAAGCACTGAGGGGGGAGG 644
 553 CTGTGGAGACCAAGCATCTGCTTGTAAAGAAAGCAAGATGATGATGATGATGATGATG 612
 645 CTGTGGAGACCAAGCATCTGCTTGTAAAGAAAGCAAGATGATGATGATGATGATGATG 704
 613 ACAACCAATCTCCCTTGGAAACAGATACAGATTTCTTCAAGGGGACAGCATTTGGGG 672
 705 ACAACCAATCTCCCTTGGAAACAGATACAGATTTCTTCAAGGGGACAGCATTTGGGG 764
 673 TTTTCTAGAGTGTGCG-----AGATTAACCTGATGAGAGCTGTAGAGCATCCCG 723
 765 TTTTCTAGAGTGTGCGCAACACAGAAAGAAACAAAGGAGCTGTAGAGTGTGCA 824
 724 GTGACTGAGAGAGTGAAGTGTGCGTGTTCAGCTGACCCCATATTTACATTCCTGGGC 783
 825 GTGACTGAGAGAGTGAAGTGTGCGTGTTCAGCTGACCCCATATTTTCTTACTTGTGGC 884
 784 AATGACTGATCCGACGCGAAGGAGAGATTTGCTTTCAGAGACAGATGCTCCCATC 843
 885 AGGACTGATCCGACGCACTAAGAGAAAGTGTGTCTGCGCCACAAACAGAGCTCCCTTC 944
 844 CCTCCAGATGACAAAGACGATGCTGGAGGCTGTGCTCTCTCTCTCTCTCTCTCTCTCT 900
 945 CCTCTGATTAACAAAGAAAGCGGAGGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1004
 901 CTGTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 960
 1005 CTGTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1064
 961 ACAGAAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020

Db 1065 AAGAGACTTCTTTTCTA---CCACCACATATGCCCCCATTAAGGTTCTGTGTT 1121
 1021 TATCTCTTGTAGATATGTTTCCATTCACACCGTGTGCTTCACTGATCTTTCTTCAAAAC 1080
 1122 TACCATCTGAATATGTTTCCATTCACCAATTTGTACTTACTTCAATTTCTTCAAAAC 1181
 1081 TACTGAGAAAGTGAAGTCACTCTTGAATAAATGACAGAAAGAAATTCGCCAGATGGGG 1140
 1182 CATTCGAGAAAGTGAAGTCACTCTTGAATAAATGACAGAAAGAAATTCAGAGATGGGT 1241
 1141 CCGTCAAGTGTGACACCTGAGAGCAAGCGGAGATTAAGTGTGCTTCTCTTCTCC 1200
 1242 CAGTCAAGTGTGACACCTGAGAGCAAGCGGAGATTAAGTGTGCTTCTCTTCTCC 1301
 1201 AGTGAAGTGTGACACCTGAGAGCAAGCGGAGATTAAGTGTGCTTCTCTTCTCC 1260
 1302 AATGAGTGTGACACCTGAGAGCAAGCGGAGATTAAGTGTGCTTCTCTTCTCC 1361
 1261 AACTCTAGAGATGTGTTCCCTTGTGCTTAACTCTTTGTAGTATTTCAAGAGCCAG 1320
 1362 AACTCTAAGA-CTTCTCCCTGCTTAACTTTCTGAGTGTCTAAGAAAGCCAG 1420
 1321 AGCATCTGCAAAATACCTGTGTGTCTATCTTTGGGGAGAGCACTCAAGGCACTAT 1380
 1421 ATTCATCTGCAAAATACCTGTGTGTCTATCTTTAGAGATTTGATCAAAAGCGATTAC 1480
 1381 AATGCTGTGAGTGTGCTGCCCCCAATATCATCTCATGAAGAGCGCCAGCTTTCCACACA 1440
 1481 AATGCTGTGAGTGTGCTGCCCCCAATATCATCTCATGAAGAGCGCCAGCTTTCTGTGA 1540
 1441 GAACTTCTGAAGCTTACGAGAGATGTGATGAAGAAAGCTCACAGCTTCCATGAT 1500
 1541 GAACTTCTGAAGCTTACGAGAGATGTGATGAAGAAAGCTCACAGCTTCCATGAT 1600
 1501 AGCTTTCACCTCTTGTATGTCACCCGGGGAA--TGAACCTCTGAAGCTTCTTACTT 1558
 1601 GGTGTGTCTCTTGTGAGCCACCATGAGAGCAAGAACCTTAAAGGCTTCTTATCC 1660
 1559 CCCTTCAGTGAACATGCTGTGTGAGCACTGAA 1594
 1661 ACCAATTACAGGAAAGAAAGCTGTATGATCTGAA 1696

RESULT 10
 AA52046
 ID AA52046 strand: cDNA; 1918 BP.
 XX AC
 XX AA52046;
 XX AC
 XX 09-AUG-2000 (first entry)
 XX AC
 XX DE cDNA encoding interleukin 17-like receptor protein (IL17RLP)-2.
 XX AC
 XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
 XX resistant chronic infection; acute infection; mycobacterial infection;
 XX T-cell proliferation; IL-2 biosynthesis; lymphocytic leukemia;
 XX T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 XX IL-6 expression; myeloma; plasmacytoma; Lemmer's lymphoma;
 XX Immunoprotective; cytosolic; hematopoietic; proliferative;
 XX antibacterial; ss.
 XX AC
 XX OS Homo sapiens.
 XX AC
 XX FH Key Location/Qualifiers
 XX FT 111..1412
 XX FT /*tag= a
 XX FT /product= "Interleukin-17 like receptor protein"
 XX AC
 XX PD MO200015759-A1.
 XX AC
 XX PD 23-MAR-2000.
 XX AC
 XX PF 15-SEP-1999; 99WO-US21048.

Db 601 ACAACCACTCCCTGGGAAACAGATACATAGCGCTTATCCAAACAGCACTATCATCG33 660
 Qy 673 TTTTCTAGAGTCTG3-----AGAAATAACTGATGAGAGCGTCTAGCCATCCG 723
 Db 661 TTTTCTAGAGTCTG3-----AGAAATAACTGATGAGAGCGTCTAGCCATCCG 720
 Qy 724 GTGACTGAGAGAGTGAAGGTGGTGTGCTGAGTGAACCCCATATTTTACATCTGG33 783
 Db 721 GTGACTGAGAGAGTGAAGGTGGTGTGCTGAGTGAACCCCATATTTTACATCTGG33 780
 Qy 784 AATGACTGATCCGAGCGCAAGAGGAGAGTGTGCTTGTCTGAGAGCAAGTGTCTCCATC 843
 Db 781 ACCGACTGATCCGAGCAATAGAGAGAGTGTGCTTGTCTGAGAGCAAGTGTCTCCATC 840
 Qy 844 CCTCAGATGACAAACAGAGCAAGTGTGAGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCT 900
 Db 841 CCTCAGATGACAAACAGAGCAAGTGTGAGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCT 900
 Qy 901 CTGTGTGCTGT 960
 Db 901 CTGTGTGCTGT 960
 Qy 961 AGAAGAGCT 1020
 Db 961 AGAAGAGCT 1017
 Qy 1021 TATCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Db 1018 TATCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
 Qy 1081 TACTGAGAGAGTGAAGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
 Db 1078 CATGTGAGAGAGTGAAGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1137
 Qy 1141 CCGGTACAGT 1200
 Db 1138 CCGGTACAGT 1197
 Qy 1201 AGTGAAGT 1260
 Db 1198 AGTGAAGT 1257
 Qy 1261 AACTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 Db 1258 AACTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
 Qy 1321 ACCGATCTGCAAAATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
 Db 1318 ACCGATCTGCAAAATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1377
 Qy 1381 AATGCTGAGT 1440
 Db 1378 AATGCTGAGT 1437
 Qy 1441 GAATCTCTGCAAGGCTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
 Db 1438 GAATCTCTGCAAGGCTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1497
 Qy 1501 AGCTGTCTACCTGT 1518
 Db 1498 AGCTGTCTACCTGT 1515
 RESULT 12
 AAS09514
 ID AAS09514 standard; CDNA; 1515 BP.
 XX
 AC AAS09514;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human CDNA encoding Interleukin 17 receptor, IL-17RH1.

XX
 KW Human; Interleukin-17 receptor; IL-17RH1; agonist; antagonist; ss;
 KW PRO5801; DNA 115291-2681; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KW allergic disease; asthma; demyelinating disease;
 KW degenerative cartilaginous disorder; transplantation associated disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 7..1515
 FT /tag= a
 FT /product= "IL-17RH1"
 FT sig_peptide 7..48
 FT /tag= b
 FT mat_peptide 49..1512
 FT /tag= c
 FT /label= Mature_IL_17RH1
 PN WO200146420-A2.
 PD 28-JUN-2001.
 PF 20-DEC-2000; 2000WO-US34956.
 XX
 PR 23-DEC-1999; 99US-0172096.
 PR 30-DEC-1999; 99WO-US31274.
 PR 11-JAN-2000; 2000US-0175481.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 21-MAR-2000; 2000US-0191007.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 22-JUN-2000; 2000US-0213087.
 PR 22-AUG-2000; 2000US-0644848.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 24-OCT-2000; 2000US-0242837.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-0253646.
 PR 01-DEC-2000; 2000WO-US32678.
 XX
 PA (GENENTECH INC.
 XX
 PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;
 PI Macanabe CK, Williams PM, Wood WI, Yansura DG;
 XX
 DR WPI; 2001-451708/48.
 DR P-PSDB; AAU04955.
 XX
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 PT arthritis and diabetes -
 XX
 PS Claim 1; Fig 11; 188pp; English.
 XX
 CC The sequence (DNA 115291-2681) encodes a PRO polypeptide (PRO5801)
 CC which is the human interleukin 17 receptor, IL-17RH1. A composition
 CC containing ant/agonists to the PRO polypeptides or individual components
 CC are useful for treating a mammal with an immune related disease, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
 CC disease, contact dermatitis, an allergic disease e.g. food
 CC hypersensitivity, asthma, a transplantation associated disease, or a
 CC chronic inflammatory demyelinating polyneuropathy. Treating a
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 CC examples of the diseases and disorders are given in the specification.
 XX

Sequence 1515 BP; 404 A; 384 C; 363 G; 364 T; 0 other;

Query Match 49.1%; Score 963.6; DB 22; Length 1515;
Best Local Similarity 78.7%; Pred. No. 6.8e-285;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

QY 13 CCGGCCATGTTGCTAGTGTGCTGATCTTGGCTGATCTGTCAGAGAGAGCCCTGCTGCA 72
DB 1 CCGGCCATGTTGCTAGTGTGCTGATCTTGGCTGATCTGTCAGAGAGAGCCCTGCTGCA 60
QY 73 GAGCCGACTATTCAGTGTGCTGAGCAGAGGACATCTCCAGAGTGGATGGTCCACAC 132
DB 61 GAGCCGACTATTCAGTGTGCTGAGCAGAGGACATCTCCAGAGTGGATGGTCCACAC 120
QY 133 ACACCTACTCCAGAGACTTGAAGGACCTCCAGTGAACCTGCTCAAGACAAAGTGGCA 192
DB 121 GATCTAATCCCGGAGACTTGAAGGACCTCCAGTGAACCTGCTCAAGAGTGGCA 180
QY 193 GCAGAGAGATTTCAATTTTATGACATTAAGCTGATCTCCGGGAGAGCCGACATC 252
DB 181 ACAGGGGACTATTCATTTGATGAATGTAAGTGGTACTCCGGGAGATGCCAGATC 240
QY 253 CGCTTTGTAAGGACACAGATCTGGTGAAGGCAAAAACAATGAATTCATAGC 312
DB 241 CGCTTTGTAAGGACACAGATTTGTGACGGGCAAAACCACTTCCAGTCTAGAC 300
QY 313 TGTGTAGTGTCACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGGCAAA 372
DB 301 TGTGTAGTGTCACTACACAGAGGCTTCCAGTCAAGACAGACCTTCCGGGCAAA 360
QY 373 TGAACATTTCTCTATGAGGCTTCCCTGTGAGCTGACACTCTCTATCTCATAGGCC 432
DB 361 TGAACATTTCTCTATGAGGCTTCCCTGTGAGCTGACACTCTCTATCTCATAGGCC 420
QY 433 CATTAACATCCCAATGCTAATATGATGAGACAGACCTTCTTGTGCTGAATTCACC 492
DB 421 CATTAATTTCTCTAATGCAAAATATGATGAGATGGCCCTTCTCATGTCTGTAATTCACC 480
QY 493 TCGCCAGGCTGCTTAAACAAGTATGATAATATTAAGACAGTCACTGAGCGGGAAGC 552
DB 481 TCAACAGGCTGCTTAAACAAGTATGATAATATTAAGACAGTCACTGAGCGGGAAGC 540
QY 553 CTGTGGGACCCAGACATCACTGCTTTGTAAGAAAGACAGAAAGATGTTGAATTC 612
DB 541 CTGTGGGATCCGAACATCACTGCTTTGTAAGAAAGATGAGACAGATGAAGTAACTTC 600
QY 613 ACAACCAATCCCTTGAAGACAGTACAGATCTCATTAAGGGGACAGACATTTGGGG 672
DB 601 ACAACCAATCCCTTGAAGACAGTACAGATCTCATTAAGGGGACAGACATTTGGGG 660
QY 673 TTTTCTAGATGTGCTG-----AGAAATAACTGATGAGAGCTGTAGCCATCCG 723
DB 661 TTTTCTAGATGTGCTGAGCCACACAGAAAGAAACAAGGAGCTTCAAGTGTATCCA 720
QY 724 GTGACTGAGAGAGTGAAGTGGCGGTTCAGCTGACCCCATATTTAATACCTGCGGC 783
DB 721 GTGACTGAGAGATGTAAGTGGCGGTTCAGCTGACCCCATATTTAATACCTGCGGC 780
QY 784 AATGATGATCCGACGCGAGAGGAGAGTGTGCTTGTCAAGAGACAATGCTCCCATC 843
DB 781 AGGAGCTGATCCGACATTAAGAGAGAGTGTGCTTGTCCACAAAGAGCGCTCTTC 840
QY 844 CTTTCAAGTACAAACAGACCATGCTGGAGGCTGCTGCTCTCTTCTGCTGCTG---CTG 900
DB 841 CTTTCTGATTAACAACAAAGACAGCGGAGGCTGCTGCTCTCTCTGCTGCTGCTG 900
QY 901 CTGTGGCTGTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 CTGTGGCTGTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 AGAAGAGCTCTTCTCTATTTTCCACATGCTCTGCTCCCTCATTTAAGCTCGTGGT 1020
DB 961 AAGAGAGCTCTTCTCTATTTTCCACATGCTCTGCTCCCTCATTTAAGCTCTGCTGGT 1017

QY 1021 TATCTTCTGAGATATGTTTCCATCAACCGTCTGCTTCACTGACTTTCTTCAAAAC 1080
DB 1018 TACCACTCTGAATATGTTTCCATCAACAACTTTGTTACTTCACTGAATTTCTTCAAAAC 1077
QY 1081 TACTGCAAGAGTGAAGTCACTCTTGAAGAAATGGCAGAAAGAAATGCCCGGAGTGGG 1140
DB 1078 CATTTGCAAGAGTGAAGTCACTCTTGAAGAAATGGCAGAAAGAAATGACAGATGGT 1137
QY 1141 CCGTACAGTGTGCTGACCACTGAAAGCAAGCGGAGATTAAGTGTCTTCTTCTCC 1200
DB 1138 CCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
QY 1201 AGTACGTCTCCGACCTTGTGTGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1198 AATGAGCTCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1257
QY 1261 AACTCTCAGATGTGTTCTCTCTGCTTAACTCTTTTGTAGTATTTGACAGCCAG 1320
DB 1258 AACTCTCAGATGTGTTCTCTCTGCTTAACTCTTTTGTAGTATTTGACAGCCAG 1317
QY 1321 ACCATCTGCAAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1318 ATTCATCTGCAAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1377
QY 1381 AATGCCCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1378 AATGCTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1437
QY 1441 GAACCTTCTCAAGCTACGACAGAGATGTCAGTGAAGAAACGCTCAACAGCTGCTGAT 1500
DB 1438 GAACCTTCTCAAGCTACGACAGAGATGTCAGTGAAGAAACGCTCAACAGCTGCTGAT 1497
QY 1501 AGCTGTTCACCTTGTAG 1518
DB 1498 GGTCTGCTGCTCTTGTAG 1515

RESULT 13
AAF92136
ID AAF92136 standard; cDNA; 1515 BP.
XX
AC AAF92136;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PROS801 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23328.
XX
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 07-DEC-1999; 99US-0169495.
PR 09-DEC-1999; 99US-0170262.
PR 11-JAN-2000; 2000US-0175481.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 03-MAR-2000; 2000US-0187202.
PR 25-APR-2000; 2000US-0199397.
PR 22-MAY-2000; 2000WO-US14042.
PR 05-JUN-2000; 2000US-0209832.
XX
PA (GETH) GENENTECH INC.

KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 10..1290
 FT /*tag= a
 FT /product= "interleukin 17-receptor-like protein"
 FT sig_peptide /product= b
 FT /tag= b
 FT mat_peptide 67..1287
 FT /*tag= c
 FT
 PN WO200055204-A1.
 PD 21-SEP-2000.
 PF 06-MAR-2000; 2000MO-US05759.
 PR 16-MAR-1999; 99US-0268311.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Shi Y, Ruben SM;
 DR WPI; 2000-647065/62.
 DR P-PSDB; AAB18750.
 XX
 PT Novel gene encoding a polypeptide of the interleukin-17 receptor
 PT family, and an antagonist and agonist of the polypeptide, useful for
 PT treating, diagnosing, detecting and/or preventing immune system related
 PT disorders -
 XX
 PS Claim 2; Fig 1A-C; 247pp; English.
 CC The present sequence encodes a human interleukin 17-receptor-like
 CC protein (IL17R). The IL17R polypeptide is useful for screening for
 CC agonists and antagonists. These antagonists and agonists are useful for
 CC treating, diagnosing, detecting and or preventing disorders related to
 CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
 CC cellular migration, ovulation or neurogenesis, such as osteoporosis,
 CC arthritis and autoimmune disorders e.g. systemic lupus erythromatosus.
 XX
 SQ Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
 Query Match 49.1%; Score 963.6; DB 21; Length 1816;
 Best Local Similarity 77.4%; Pred. No. 7.6e-285;
 Matches 1236; Conservative 1; Mismatches 340; Indels 19; Gaps 5;

QY 373 TGGACATTCCTATGAGGCTTCCCTGAGAGCTGAGACCTCTATCTCATCAGCGCC 432
 DB 364 TGGACATTTTCTTACATCGGCTTCCCTGTAGAGCTGACACAGCTATTTCAATGGGGCC 423
 QY 433 CATTAATCCCAATGCTATATGAATGAGACAGCCCTTTCTGTGTGAATCTTACC 492
 DB 424 CATTAATTCCTTAATGCAATATGAATGAGAGGCGCTTCAATGTCTGTGAATTTTACC 483
 QY 493 TCGCAGGCTGCTTAACCAAGTATGAATATTAAGAGAGTGCATGAGGCGGAGC 552
 DB 484 TCACAGGCTGCTTACACCATATATGAATATTAAGAGAGTGCATGAGGCGGAGC 543
 QY 553 CTGTGGACCCAGACATCACTGCTTTAAAGAGAGAGAGTGTGAATGAATTTT 612
 DB 544 CTGTGGATCCGAACATCACTGCTTTAAAGAGAGAGAGTGTGAATGAATTTT 603
 QY 613 ACAACCAATCCCTTGGAAACAGATACAGATTTCTATTCACAGGAGACAGCATTTGGG 672
 DB 604 ACAACCAATCCCTTGGAAACAGATACAGATTTCTATTCACAGACATATCATGAGG 663
 QY 673 TTTTCTAGAGTGTGG-----AGAAATAACTGATGAGAGCTGTAGGCATCCG 723
 DB 664 TTTTCTAGAGTGTGGAGCAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723
 QY 724 GTGACTGAG 783
 DB 724 GTGACTGAG 783
 QY 784 AATGACTGCATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
 DB 784 AAGGACTGCATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
 QY 844 CCTCAGATGACAAACAG 900
 DB 844 CCTCAGATGACAAACAG 903
 QY 901 CTGTGGCTGTGTGGAG 960
 DB 904 CTGTGGCTGTGTGGAG 963
 QY 961 ACGAAGAGCTCTTCTTCTATTTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 964 AAGAAGAGCTCTTCTTCTA---CCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 1021 TATCCTTGAAGATATGTTTCCATCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 1021 TATCCTTGAAGATATGTTTCCATCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1081 TACTGAG 1140
 DB 1081 TACTGAG 1140
 QY 1141 CCGGTACAGTGTGTGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 DB 1141 CCGGTACAGTGTGTGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1201 AAGTACAGTGTGTGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 AAGTACAGTGTGTGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 AACTCTCAGAGATCTTCCCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 AACTCTCAGAGATCTTCCCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1318
 QY 1321 ACGCATCTGACAAATACCTGTGTGTATCTTTGGGAGAGAGAGAGAGAGAGAGAGAG 1380
 DB 1319 AATCATCTGACAAATACCTGTGTGTATCTTTAGAGAGAGAGAGAGAGAGAGAGAGAG 1378
 QY 1381 AATGCTCAGAGTGTGAG 1440
 DB 1379 AATGCTCAGAGTGTGAG 1438

Oy	1441	GACCTTCGCAAGGTAGCAGCAGCATGTCAGTGAAGAAGCGCTCACAAACCTCCATCAT	1500
Dd	1439	GAACTTTCTTCATGTGCATGACGAGGTCTGACGAGAAAAAAGATCAACAACCTGGCAGAT	1498
Oy	1501	AGCTGTTACCCCTTGTAAGTCACCACCGGGGAAA--TAGAGACTCTGAAGCCTTCTACTCT	1558
Dd	1499	GGCTGCTGCTCTCTTGTATGCCACCCAGAACGAAAGMGACCTTAAGGCTTCTATCCC	1558
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RESULT: 15			
ID	AAZ52035	standard; cDNA; 1816 BP.	
XX	AAZ52035;		
XX	AAZ52035;		
DT	09-AUG-2000	(first entry)	
De	cDNA encoding interleukin 17-like receptor protein (IL17RLP)-1.		
XX			
KW	Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;		
KW	resistant chronic infection; acute infection; mycobacterial infection;		
KW	T-cell proliferation; IL-2 biosynthesis; lymphocytic leukemia;		
KW	T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;		
KW	IL-6 expression; myeloma; plasmacytoma; Lennert's lymphoma;		
KW	immunoprotective; cytostatic; hematopoietic; proliferative;		
KX	antibacterial; ss.		
OS	Homo sapiens.		
XX			
XX			
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PN	WO200015759-A1.		
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XX	23-MAR-2000.		
XX			
PE	15-SEP-1999;	99MO-US21048.	
XX			
PR	16-SEP-1998;	98US-0154219.	
PR	16-SEP-1998;	98MO-US19121.	
PR	16-MAR-1999;	99US-0268311.	
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
P1	Ruben SM, Shi Y;		
XX			
WI	2000-271403/23.		
DR	P-Psdb; AAY70591.		
XX			
PT	Novel polynucleotides encoding interleukin-17-like receptor protein,		
PT	useful for diagnosis and treatment of immune system-related disorders,		

PT	e.g. sepsis and cancers -
XX	
PS	Claim 2; Fig 1; 147bp; English.
CC	The patent relates to novel interleukin-17-like receptor
CC	protein (IL-17R). IL-17R is a homologue of the IL-17 receptor and has
CC	a wide range of cytokine receptor-like activities. IL-17R or its
CC	agonists may be used to enhance host defenses against resistant chronic
CC	and acute infections, e.g. mycobacterial infections, via the attraction
CC	and activation of microbicidal leukocytes. It may also be used to
CC	increase T-cell proliferation by stimulating IL-2 biosynthesis, for the
CC	treatment of T-cell mediated autoimmune diseases and lymphocytic
CC	leukemias. IL-17R may also be used to regulate hematopoiesis and to
CC	treat sepsis. Extracellular IL-17R domains may be used as antagonists
CC	of IL-17R. IL-17R agonists and antagonists can also be used to
CC	modulate IL-6 expression, useful in treatment of cancers such as
CC	myelomas, plasmacytomas and hybridomas and Lemmer's Lymphoma. The
CC	present cDNA sequence encodes human IL-17R. This cDNA sequence was
CC	discovered in a cDNA library derived from human adult pulmonary tissue.
XX	
SQ	Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
Query Match	49.1%; Score 963.6; DB 21; Length 1816;
Best Local Similarity	77.4%; Pred. No. 7.6e-285;
Matches 1236; Conservative	1; Mismatches 340; Indels 19; Gaps 5
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Dd	64 GAGCGCACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAATGTGATCAACAAT 123
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Dd	364 TGACATATTTCTTACATCGGCTTCCCTGTGAGCTGAGACACAGTCTATTTCAATGGGGCC 423
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Dd	484 TCACCAAGGCTGCTTAAGACCAATATATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAC 543
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Db 1559 ACCAATTACAGGAGAAAGAGTGTGTGATCTGTGA 1594

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Job time : 412.851 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:37:09 ; Search time 4999.22 Seconds

(without alignments)
11427.544 Million cell updates/sec

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Perfect score: 1963
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	989.8	50.4	1818	6	AX191534 Sequence
6	988.2	50.3	1841	6	AX253204 Sequence
7	988.2	50.3	1841	6	AX365258 Sequence
8	985.8	50.2	2042	9	BC000980 Homo sapi
9	983	50.1	1796	6	AX350967 Sequence
10	980.8	50.0	1828	9	AF208110 Homo sapi
11	971.2	49.5	1583	9	AF250309 Homo sapi
12	964	49.1	1816	9	AF212365 Homo sapi
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14	963.6	49.1	1515	6	AX180774 Sequence
15	963.6	49.1	1515	6	AX376332 Sequence
16	960.8	48.9	1509	6	AX191524 Sequence
17	912.6	41.4	1506	6	AX350969 Sequence
18	765.8	39.0	2015	6	AX253207 Sequence
19	765.8	39.0	2015	6	AX365260 Sequence
20	752.6	38.3	1701	6	AX061651 Sequence
21	751	38.3	1713	6	AX253209 Sequence
22	632.2	32.2	637	6	AX350970 Sequence
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31	44.2	2.3	3120	9	HSU58917 Homo sapien
32	44.2	2.3	3223	6	AR034066 Sequence
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37	44.2	2.3	3223	6	AR131081 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Mus musculus IL-17 receptor homolog precursor (Evi127) mRNA,
complete cds.
ACCESSION AF208108
VERSION AF208108.1 GI:9246428
KEYWORDS
SOURCE
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1963)
Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.
and Staughtness, J.D., Jr.

TITLE Evi27 encodes a novel membrane protein with homology to the IL17 receptor

JOURNAL Oncogene 19 (17), 2098-2109 (2000)

MEDLINE 20273223

PUBMED 10815801

REFERENCE 2 (bases 1 to 1963)

AUTHORS Snaughnessy,J.D. Jr.

JOURNAL Direct Submission

Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W. Markham St, Little Rock, AR 72212, USA

FEATURES

source Location/Qualifiers

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1300. .1305

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1178. .1182

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Best Local Similarity 100.0%; Pred.No. 0;

Matches 1963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTGGCCAGTGCCGGGCGCATGTTGCTAGTGTGCTGATCTTGCTGCATCTGTCAGAGAC 60

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QY 421 CTGATAGGCGCCATTAACATCCCAATGCTATATGATAGAGACAGCCCTTTGTCT 480

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DB 661 ACACATTGGGGTTTCTAGAGTGTGAGAAATTAAGTGAAGAGCTGTAGCCATC 720

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DEFINITION Mus musculus, interleukin 17B receptor, clone MGC:35924
ACCESSION BC026546
VERSION BC026546.1 GI:20071644
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SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2018)

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AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-Apr-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAX Plate: 58 Row: m Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9624983.
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ACCESSION AF208109
VERSION AF208109.1 GI:9246430
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 2589)
Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.
and Shaughnessy, J.D., Jr.
Evl27 encodes a novel membrane protein with homology to the IL17
receptor
JOURNAL Oncogene 19 (17), 2098-2109 (2000)
MEDLINE 20273223
PUBMED 10815801
REFERENCE 2 (bases 1 to 2589)
Shaughnessy, J.D., Jr.
Direct Submission
JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research
Center, University of Arkansas for Medical Sciences, 4301 W.
Markham St, Little Rock, AR 72212, USA
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SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP23-25A7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 234131)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT
Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www.seq.wi.mit.edu
Contract: sequence_submissions@genome.wi.mit.edu
Project Information
Center Project name: L13729
Center clone name: 25 A 7
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Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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Consensus quality: 230172 bases at least Q30
Consensus quality: 231921 bases at least Q20
Insert size: 21000; agarose-efp
Insert size: 232831; sum-of-contents
Quality coverage: 10.4 in Q20 bases; agarose-efp
Quality coverage: 9.4 in Q20 bases; sum-of-contents

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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AUTHORS	1 (bases 1 to 1818) Kato, S. and Kimura, T.
TITLE	Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL	Patent: WO 0149728-A 56 12-JUL-2001; Proteome Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and
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Amgen, Inc. (US)
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 2042)

Strausberg, R.

Direct Submission

Submitted (16-NOV-2000) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUMI)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>Contact: villalob@bcm.tmc.edu

Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,

A.M., Hollway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,

Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLUMI at: <http://image.llnl.gov>
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CDS

Center, University of Arkansas for Medical Sciences, 4301 W.
Markham St., Little Rock, AR 72212, USA

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QY 1143 GGTACAGT 1202
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LOCUS Homo sapiens putative cytokine receptor CRL4 precursor mRNA,
DEFINITION complete cds.
ACCESSION AF250309
VERSION AF250309.1 GI:13649476
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1583)
TITLE Zhang, W. and Cao, X.
JOURNAL Direct Submission
Submitted (29-MAR-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Rd., Shanghai 200433, P.R. China
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BASE COUNT 427 a 397 c 377 g 382 t
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Query Match 49.5%; Score 971.2; DB 9; Length 1583;
Best Local Similarity 78.6%; Pred. No. 3.2e-282;
Matches 1204; Conservative 0; Mismatches 313; Indels 15; Gaps 3;

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QY 139 ACTCCAGAGACTGTGAGGAGACCTCCAGATGGAACCTGTCAAGACAGTGTGACAGAG 198
Db 121 ATCCCGAGAGACTGTGAGGAGACCTCCAGATGGAACCTGTCAAGATGTGTGACAGAG 180
QY 199 GAGTTTCAATTTTGTATGAACAATAGCTGATATCTCCGCGCAGACCGCATCCGCTTG 258
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QY 259 TTGAAAGGCCACCAAGATCTGCGCTGAGTGGCAAAAACAATGAATTCAACAGCTGTGTG 318
Db 241 TTGAAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCAGTCTTACAGCTGTGTG 300
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Db 1318 ATTCACTGTGACAAATAGGTGTGTCTACTTTAGAGAGATTGATACAAAAGCGATTAC 1377
Qy 1381 AATGCCCTGAGTGTCTGCCCCCAATATCTCATGAGAGAGCGCCACAGCTTTCACACA 1440
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Qy 1501 AGCTGTTCAACCCCTTGTAG 1518
Db 1498 GGCTGCTGCTCTTGTAG 1515

Search completed: May 28, 2003, 06:56:38
Job time : 5282.72 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using SW model

Run on: May 27, 2003, 23:21:54 ; Search time 3594.88 Seconds

(without alignments)
11663.832 Million cell updates/sec

Title: US-09-778-971-4

Perfect score: 2589
Sequence: 1 gtggccagtcgcccgcacat.....aaaaaaaaaaaaaaaaa 2589

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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15: em_estfun:*
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17: gb_gss:*
18: em_gss_hum:*
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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	24.3	728	10	BB667509
2	624	24.1	678	10	BB307800
3	502.4	19.4	646	10	BB644125
4	489.4	18.9	773	13	BT103740
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9	366.8	14.2	370	9	AA562342
10	366	14.1	652	14	BM693867
11	360	13.9	518	9	AT616016
12	357.4	13.8	908	9	AL565993
13	353.6	13.7	551	12	BG384365
14	352.2	13.6	523	10	BB284760
15	352	13.5	588	13	B1360842
16	349.2	13.5	946	13	B1823321
17	348.6	13.5	561	10	AW675096
18	333.2	12.9	676	10	AV727345
19	330.2	12.8	680	10	AM970151
20	313.2	12.1	572	13	BM030860
21	305.4	11.8	869	9	AL535617
22	301.6	11.6	340	10	BB165105
23	291.8	11.3	299	9	AT505977
24	290.4	11.2	304	9	AT615611
25	286.8	11.1	477	9	AA287951
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35	248.2	9.6	313	10	BB166664
36	244.2	9.4	703	10	AV708899
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44	221.8	8.6	250	9	AT662246
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ALIGNMENTS

RESULT 1
LOCUS BB667509
DEFINITION BB667509 RIKEN full-length enriched, adult male liver tumor Mus
ACCESSION BB667509
VERSION BB667509.1 GI:16398958
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 728)
AUTHORS Arakawa, T., Carinci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, U., Komoto, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okio, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba, Ibaraki, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
 M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

Location/Qualifiers
 1. 728
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 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5']
 GAGAGAGAGAGCGCGCGAAGTCAGTTTCTTTTCTTTTNN 3']. cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5']
 GAGAGAGATCTCGAGTTAAATTAATTAATCCGCCGCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 Bluescript KS(+) after bulk excision from Lambda PUC I.
 Tissue was provided by William A. Held, Roswell Park
 Cancer Institute, Department of Molecular and Cellular
 Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose
 assistance we gratefully acknowledge."

BASE COUNT 189 a 180 c 167 g 188 t 4 others

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 Matches 658; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

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RESULT 2
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 ACCESSION BB307800.2 GI:15411368
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 678)
 AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
 Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel.: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh


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Db 362 TCCGCGGCAAGCATGACATCTCTATGATAGCTTCCCTGAGGAGTGAGACACT 421
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RESULT 6
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LOCUS mg66101.r1 Soares_thymus_2NbmT Mus musculus cDNA clone IMAGE:583729
DEFINITION
AA144114 5', mRNA sequence.
ACCESSION
AA144114.1 GI:1713482
VERSION
AA144114.1 GI:1713482
KEYWORDS
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SOURCE
house mouse.
MUSCULUS
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 439)
REFERENCE
Mairia, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
CONTACT: Mairia M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:358377
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 430.
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3)], double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."
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QY 441 CCCCAATGCTAATATGATAGAGAGAGCCCTTCTTTGTCTGTGAATCTTACCTGCGAGG 500
Db 61 CCCCAATGCTAATATGATAGAGAGAGCCCTTCTTTGTCTGTGAATCTTACCTGCGAGG 120
QY 501 GTGCACTGTGAAAAACAAGAGTAAGTCGAGTATTTTCAGAGCTTAACAGCAGGC 560
Db 121 GTGCACTGTGAAAAACAAGAGTAAGTCGAGTATTTTCAGAGCTTAACAGCAGGC 180
QY 561 TCTCCGATTTTCAAGCTCTTCTTCCATTACATTTCTCTCTGCGCAGAGACTCAT 620
Db 181 TCTCCGATTTTCAAGCTCTTCTTCCATTACATTTCTCTCTGCGCAGAGACTCAT 240
QY 621 TCTCCGATTTTCAAGCTCTTCTTCCATTACATTTCTCTCTGCGCAGAGACTCAT 680
Db 241 TCTCCGATTTTCAAGCTCTTCTTCCATTACATTTCTCTCTGCGCAGAGACTCAT 300
QY 681 TCTCCGATTTTCAAGCTCTTCTTCCATTACATTTCTCTCTGCGCAGAGACTCAT 740
Db 301 TCTCCGATTTTCAAGCTCTTCTTCCATTACATTTCTCTCTGCGCAGAGACTCAT 360
QY 741 TATGAATCCCAAGAGGCACTGAATTTCTTCACTATGAGCCCTATCTGCGCTGTGACA 800
Db 361 TATGAATCCCAAGAGGCACTGAATTTCTTCACTATGAGCCCTATCTGCGCTGTGACA 420
QY 801 TTGTTGGTGAGGCTGTGC 819
Db 421 TTGTTGGTGAGGCTGTGC 439

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RESULT 7
BF322373/c 431 bp mRNA linear EST 21-NOV-2000
LOCUS ma24a07.x1 NCI_CGAP_L110 Mus musculus cDNA clone IMAGE:3811861 3',
DEFINITION
BF322373 mRNA sequence.
ACCESSION
BF322373.1 GI:11271749
VERSION
BF322373.1 GI:11271749
KEYWORDS
EST.
SOURCE
house mouse.
MUSCULUS
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
MGI:1453973
Seq primer: -40UP from Gibco
High quality sequence stop: 367.
Location/Qualifiers
1. .431
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3811861"
/clone_lib="NCI_CGAP_L110"
/sex="female"
/dev_stage="10 weeks"
/lab_host="DH10B (TI phage-resistant)"
/Note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT."
FEATURES
source

```


Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 370)
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Marris, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenger, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marris/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu

FEATURES
 source
 1. .370
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:973013"
 /clone_1ib="Stratagene mouse Tcell 937311"
 /tissue_type="Tcell"
 /dev_stage="M30 CD4+ cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: blood; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
 Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG
 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

BASE COUNT 105 a 73 c 91 g 101 t
 ORIGIN

Query Match 14.2%; Score 366.8; DB 9; Length 370;
 Best Local Similarity 99.5%; Pred. No. 3.4e-64;
 Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2212 GACTGCAAAATGTGTGGAGAGGCTGTGTGAGGTAGTCTATGATCAAACTTGCTTTAA 2271
 1 GACTGCAAAATGTGTGGAGAGGCTGTGTGAGGTAGTCTATGATCAAACTTGCTTTAA 60
 2272 AACTGAGTTTGGAAAGTCAACCTGAGCATACACGCTGAGGCTAGTCATTTGCTGATT 2331
 61 AACTGAGTTTGGAAAGTCAACCTGAGCATACACGCTGAGGCTAGTCATTTGCTGATT 120
 2332 TATGAAGACACACAGTTAAGACATTAATGAGTGGAGCACTTAATTTGGATATACCCAA 2391
 121 TATGAAGACACACAGTTAAGACATTAATGAGTGGAGCACTTAATTTGGATATACCCAA 180
 2392 AGCTGGATATGATTAATCACTGAGAACCCAGCACTCTGGCCATGAAGTAATACGGCACTT 2451
 181 AGCTGGATATGATTAATCACTGAGAACCCAGCACTCTGGCCATGAAGTAATACGGCACTT 240
 2452 CCTGTGAGGCTGTGTGAGGTTGGTCTGTCTTGACATGCCCATGCTCTATAGTGCAC 2511
 241 CCTGTGAGGCTGTGTGAGGTTGGTCTGTCTTGACATGCCCATGCTCTATAGTGCAC 300
 2512 GTTGAACCGTTTGTAACTTTAATCTGTTAATGAATATCGTTTGGGAAGCTTCAAA 2571
 301 GTTGAACCGTTTGTAACTTTAATCTGTTAATGAATATCGTTTGGGAAGCTTCAAA 360
 2572 AAAAAAAAAA 2581
 361 AAAAAAAAAA 370

RESULT 10
 LOCUS BM693867 652 bp mRNA linear EST 26-FEB-2002
 DEFINITION UI-E-DWI-ane-1-22-0-UI.r1 UI-E-DWI Homo sapiens cDNA clone
 VERSION UI-E-DWI-ane-1-22-0-UI 5', mRNA sequence.
 ACCESSION BM693867.1 GI:19007125
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 652)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M3 Reverse.

FEATURES
 source
 1. 652
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-DWI-ane-1-22-0-UI"
 /clone_1ib="UI-E-DWI"
 /tissue_type="lens"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-DWI is a normalized cDNA library containing the
 following tissue(s): lens. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CGATTAGCGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."

BASE COUNT 188 a 167 c 135 g 162 t
 ORIGIN
 Query Match 14.1%; Score 366; DB 14; Length 652;
 Best Local Similarity 76.0%; Pred. No. 4.2e-64;
 Matches 465; Conservative 0; Mismatches 145; Indels 2; Gaps 1;

1591 AGACGCTCTTCTTCAATTCACACAGCTCTGCCCCCTATTAAAGTCTGCTGGTTATC 1650
 1 AGAAGCTTCTCTTCTTCAATTCACACAGCTCTGCCCCCTATTAAAGTCTGCTGGTTATC 60
 1651 CTTCGAGATATGTTTCATCAGACACGCTGCGCTTCAAGACTTCTTCAAACTACT 1710
 61 CATCTGAATATGTTTCATCAGACACGCTGCGCTTCAAGACTTCTTCAAACTACT 120
 1711 GCAGAGTGAGGTCAATCTTGAATAATGGCAGAAAAAATATCCGAGATGGGCGCG 1770

RESULT 11	LOCUS	DEFINITION
AI616016	AI616016	518 bp mRNA linear EST 21-APR-1999 mg6b01.v1 Soares thymus_2nbwt Mus musculus CDNA clone IMAGE:583729 5' mRNA sequence.

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:583729"
/clone_1ib="Soares_thymus_2NBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
note=Vector: pRT73D-Pac (pharmacia) with a modified

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Query Match	13.9%;	Score 360;	DB 9;	length 518;
Best Local Similarity	-96.8%;	Pred. No. 7.4e-63;		
Matches 420;	Conservative 0;	Mismatches 7;	Indels 7;	Gaps 5;

AL565993/c	908 bp	mRNA	linear	EST 16-FEB-2001
LOCUS	AL565893			
DEFINITION	AL565893 LTI FL013 Fbrn1 Homo sapiens cDNA clone CS0DF016YG03 3 prime, mRNA sequence.			

ACCESSION	AL565393	
VERSION	AL565393.1	GI:12917920
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayres, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Genoscope	
	Genoscope - Centre National de Sequencage	
	BP 191 91006 EVRY cedex - France	
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	
FEATURES	Location/Qualifiers	
source	1..908	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	

BASE COUNT 225 a 172 c 223 g 259 t 29 others
ORIGIN

Query Match	13.8%;	Score 357.4;	DB 9;	length 908;
Best Local Similarity	70.4%;	Pred. No. 2.1e-62;		
Matches 544; Conservative	22;	Mismatches 195;	Indels 12;	Gaps 7;

Oy	1457	AAGGCTCCCAATCCCTCCAGATGGACAACAAACCAGTGTGGAGAGCTG--GCTGCCTCT	1515
Db	903	AACAGCGTCCTTTCCCTMAGAATTACACAAACAAAGCAGGCCGAGGCTGCTCTCCCTCMCC	844
Oy	1516	TCTGTGTCTGTCTGTGTGGCTGTGTGGTGCTGGCAGCTGGAGTTACTTACTTGGAGGC	1575
Db	843	HGCTGTCTGTCTGTGTGGCCAATGGGTGTGGTAGGAGATCTTAATGTGAAGGC	784
Oy	1576	AAGGAAGAGACAGCAAGACGCTTCCTCTAATTTTCAACANAGCTCCGGCCCCCATTAAG	1635
Db	783	AMGAAAGATTAAGAAAGACTTCATTTTCTA--CCMCACACTACGCCCCCMTTAAG	727
Oy	1636	TCCTGTGTATTATCCTTGTGAATATGTTTTCATACACCGTGTGCGTTCACCTGACT	1695
Db	726	TTCTGTGTATTACCAATCTGAATAATATGTTTCATCACACANTTTGTACTCACTGAT	667
Oy	1656	TTCTTCAAACTACTGCAGAAATGAGTCACTCTTAAAAATGGCAAAAAGAAAATCG	1755
Db	666	TTCTTCAAAACATTTGGACGAAGTAGGTCACTCTTAAAAATGGSCAGAAAAGAAAATAG	607
Oy	1756	CCGAGATGGGGCGGGTACAGTGGCTGACCACTC-ABAACAGACCGCGAGTAAATGGTTC	1814
Db	606	CAGAGATGGGTOMAGTCAAGTGGCTGTGCCACTAAAAAAGACAGCASACAAATCTGTC	547
Oy	1815	TTTCCCTC---TTCCCAATGACGTCCCGACCCCTTTGTGACAGTGGCTGTGGCCACATAG	1871
Db	546	ATTCTCTCTTTTCCCAATGACAGTCAACAGTGTGTGGAGTGTACTCTGTGGCAAAGCAG	487
Oy	1872	GGCAGCGCCACGGAGAACTTCAGAGATCTGTTCCTCTTGTCTTAACTCTTTTGTAGT	1931
Db	486	GGCAGTCCCAGTAGAACCTCTCAAGACCTCTYCCCCCTTGTAACTTTCTGTGCAGT	427
Oy	1932	GATTTC-GGAGCCAGACGCATCTGCACAAATACCGTGGTGTCTAATCTTGGGGGACGA	1990
Db	426	GATTTAACGAAGCCAGTTATATCTGCACAAATACGTGTGTCTACTTTAGAGAGATTGA	367
Oy	1991	CTTCAAAAGCGACATTAATGCTCCTGAATGTCTGCCCCCAATTCATCTCATGAAGGA-CG	2049
Db	366	TACAAAAGACGATTAACAATGCTCTCAGTGTCTCCCCCAAGTACMCCTCOMTGAAGATCC	307
Oy	2050	CCACAGCTTTCCACACAGAACTTCTCAAGGCTACGACAGCATGTCTAGTAAAGAAAGCT	2109
Db	306	TCTCTGTCTTCTGTGACGAACCTTCTCCATBTGAAGGCGAGGCTGCACACAKKAAAAAGAT	247
Oy	2110	CACAAGCTGCACATGATAGCTGTTCACCTGTGAATGCCACCGGGGGGAA--TAAGAATC	2167
Db	246	CACAASCTTCCACGATGGTGTCTGCTCTCTTGAAGCCMCCCATAGAGAAGCAAGAGCYT	187
Oy	2168	TGAAGCTTCTCTACTCTCCCTTTCACATGACAAATGCTGTGTGACACACTGTAA	2220
Db	186	TAAAGSTCTCTATCCCMCCAATTAACAGGMAAAAACGTGTATATATCTTAA	134

RESULT	13
LOCUS	BG384365
DEFINITION	BG384365 551 bp mRNA linear EST 12-MAR-2001
ACCESSION	307426 MARCH 19 IG Sub scrofa cDNA 5', mRNA sequence.
VERSION	BG384365
KEYWORDS	BG384365.1 GI:13308837
SOURCE	EST.
ORGANISM	Pig.
	Sub scrofa

REFERENCE
1 (bases 1 to 551)
Fahrenkrug, S. C., Frenking, B. A., Rohrer, G. A., Smith, T. P. L., Casas, E., Stone, M., Watson, D., Grotzinger, W. H., and Grotzinger, J. R. 1990. *Journal of Geophysical Research* 95: 10,311-10,324.

TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL	Unpublished (2000)
COMMENT	Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4386
Fax: 402 762 4390
Email: emilt@emil.marc.usda.gov
Single pass sequencing. Bases called and a/c trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -minmatch 15 options.

FOLK PRIMERS
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCGCCAGTCACGACG
 Plate#: 91 row: J column: 1
 Seq primer: ATTTAGGTGACACTATG.

FEATURES	Location/Qualifiers
source	1. .551

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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: PCMV SPORTE; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      140 a      138 c      150 g      123 t
ORIGIN

```

Query Match	13.7%	Score 353.6;	DB 12;	Length 551;
Best Local Similarity	81.3%;	Pred. No. 1.4e-61;		
Matches 410;	Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0

QY	1	GTGGCCAGTGGCCGGGCAATGTTCTAGTGTTCGTATCTTGCTGCATCTGCGAGAGC	60
Db	9	GGGGGAAGTGGCCCGCGCATATTACTGTACTCTGAGCTGGCCGCGTGAGTGGGGT	68
QY	61	GGCTTGGCCCTCAGAGGCGCAATTCAGTGTGGGCTGAGAACAGGGCCATCTCCAGATGG	120
Db	69	GCCATGCTTCCAGAGCCGACCAATTCAGTGTGGGCTCTGAGCCTGGAACTGTCTCCAGAAATGG	128
QY	121	ATGTGTCAAACAACACTCATTCCAGAGACTTGAGGGACTTCAGATGAACTGTCAAG	180
Db	129	ATGTGTTCCACACAGCTCTGACCCCGAGGAGACTTGAGGGACCTCCGATGGAACCTAATAAA	188
QY	181	ACAAAGTGGGACAGACAGAGAGTTTCAATTTGATGAAACAATAAGTGTGATCTCCGGCA	240
Db	189	AGCAGAGTTGGAGTGGAGGAGCTATTCAATTTGATGAAACAATAAGTGTGATCTCCGGCA	248
QY	241	GACGCGACAGATCGCTTTGTAAGGCGCACCAAGATCTGCGTAGTGGGCAAAACAATG	300
Db	249	GATGCCAGATATCCGATTGTTGAAGGCCACCAAGATCTGTGTGACGGCGCAAGGCGAGAG	308
QY	301	AATTATATCACTGTGTGAGGTGCAATACACAGAGGCTTCCAAAGCCAAACCAAGACT	360

Db	309	CAGACCTCAGCTGGGTGAGTGCAATTACATGAGAGCCTTCAGACTCAGACGAACT	368
Qy	361	TCCGGCGGCAATGAGCATTTCTCTATGTAGAGCTTCCTGTGAGGTAGCACTCTAT	420
Db	369	TCTGGCGGCAATGAGATGTTTCTTCTACGTAGAGCTTCCAGTGTAGTGTACAGCTAT	428
Qy	421	CTCATCAGAGGCCCATTAACATCCCAATGCTATATGATGATGAGAGACAGCCTTCTTGT	480
Db	429	TTCAATTGAGGCCCATTAATATCCCCATGCAATATGAGACGAAATGAGGCCCTCTCTTGCT	488
Qy	481	GTGAACCTCACCCTGCGCAGGCTGC	504
Db	489	GTGAACCTTACTCACCAGGCTGC	512
RESULT 14			
BB284760		523 bp	mRNA
LOCUS	BB284760		linear
DEFINITION	BB284760 RIKEN full-length enriched, adult retina		Mus musculus cDNA
ACCESSION	BB284760		
VERSION	BB284760.1		GI:8985209
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Bukacynska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 523)		
AUTHORS	Komono, H., Aikawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koyama, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.		
TITLE	RIKEN Mouse ESTs (Komono, H., et al.)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Yoshinide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasakawa, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermoactivation of thermolabile enzymes by urea-lase and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Katsunui, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.etc.riken.go.jp) for further details. Location/Qualifiers 1..523 /organism="Mus musculus" /db_xref="taxon:10090" /clone_id="BB284760" /clone_jid="RIKEN full-length enriched, adult retina" /tissue_type="retina"		

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/lev_stage="adult"
/lev_host="MDH.0B"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGAGATCCAGAGGCTCTTTTCTTTTCTTTTCTTTTCTTTT
3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5'GAGAGAGAGATCTCGAGTAATTAATTAATTAATTC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. -Retina RNA was provided by Stefano Gustinich
Department of Neurobiology, Harvard Medical School, 220
Longwood Ave., Boston, MA02115, USA, whose assistance we
gratefully acknowledge."

BASE COUNT      140 a      126 c      116 g      141 t
ORIGIN
Query Match      13.6%; Score 352.2; DB 10; Length 523;
Best Local Similarity 89.8%; Pred. No. 2.8e-61;
Matches 423; Conservative 0; Mismatches 42; Indels 6; Gaps 4.

Oy 2104 AACGCTCAAGCCGCGCATGATATACCTCTTCAACCCCTTGATGTCACACCGGGGGAAATAGG 2163
Db 3 AACGGTCAAGACCCCGCCATGATATACCTGTACC--TGTTAGTCCAGCCGGGGGATAGC 60

Oy 2164 ACTCTGAAGCCCTTCTACTCTTCCCTTCCAGTACCAATGCTGTGAGACACTCTGAATG 2223
Db 61 ACTCTGAACCTTCTACTCTTCCGCTCCAGTACAGATGCTGT-TCAGGACTCTAAATTT 119

Oy 2224 TGTGGAGAGGCTGTGTGAGAGTAGTGTATGTAACAATCTGCTTTAAATACTGAGTTTG 2283
Db 120 T--GGGAGAGCTGTGTGAGATAGTGTCTATGTAACAATCTGCTTTGAAACCTGAGATTTTG 177

Oy 2284 CAAATCTCAACCTGAGACATACACGCGCTGAGGCTAGTATGATGGTGGATTTTATGAACAAC 2343
Db 178 CAAATCTCAACCGGACATACACGCTGAGGCTAAATCATTTGGTGAATTTATGAACAAC 237

Oy 2344 ACAGTTACAGACAATATATGATGAGTGGGACCTTAATTTGGGATATACCAAGCTGGGTAATG 2403
Db 238 ACAGTTACAAACAATATATGATGAGTGGGACCTTAATTTGGGATATACCAAGCTGGGTAAT 297

Oy 2404 ATTATCTAGTGAACACGACGACTCTGGCCATGAGTAATAGCGCACTTCCCTGTGAG--GC 2462
Db 298 ATTATCTAGTGAACACGACGACTCTGGCCATGAGTAATAGCGCACTTCCCTGTGAGTGC 357

Oy 2463 TGTCTGTAGAGTTGGGTCTGTCTTGTCACTATGCCATGCTCTATGTGTGACAGTATGACCGTTT 2522
Db 358 TTTCTGTAGAGTTGGGTCTGTCTTGTCACTATGCCATGCTCTATGTGTGACAGTATGACCGTTT 417

Oy 2523 TGTAACTTTTAATCTGTTAATGAATATCCGTTTGGGAGAGCTCTCAAAA 2573
Db 418 TGTAACTTTTAATCTGTTAATGAATATCCGTTTGGGAGAGCTCTCACTAA 468

RESULT 15
LOCUS      B1360842      588 bp      mRNA      linear      EST 01-AUG-2001
DEFINITION 388904 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  B1360842
VERSION    B1360842.1  GI:15056870
KEYWORDS   EST.
SOURCE     pig.
ORGANISM  Sus scrofa
           Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

```

REFERENCE

1 (bases 1 to 588)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Caeas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

JOURNAL

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 141 row: 1 column: 23
Seq primer: ATTAGGTGACCTATAG.
Location/Qualifiers

FEATURES

source

1..588
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/issue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 146 a 151 c 126 t
ORIGIN

Query Match

Best Local Similarity 81.2%; Score 352; DB 13; Length 588;

Matches 409; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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DB 47 GCGGGAAGTGGCCCGGAGTGTACTAGTGTCTGAGCCTGGCCGGCTGTGTGGGT 106
QY 61 GCCCTGCTGAGAGCCGACTATTCACTGTGCTCTGAGACAGGGCCATCTCCAGAGTGG 120
DB 107 GCCATGCTCTCCAGAGCCGACAAATTCAGTGTGCTGAGCCTGAGCTGTCTCCAGATGG 166
QY 121 ATGGTCCAAACACACTCACTCCAGAGACTTGAGGAGCCTCCAGTGAACCTGCTCAAG 180
DB 167 ATGGGTGACAGCCTCTGACCCCAAGAGACTTGAAGGACCTCCGAGTGAACCTATTAA 226
QY 181 ACAAGTGGCAGCAGAGAGATTTTCAATTTGATGAACATAAGCTGATATCCGGGCA 240
DB 227 AGCAGTGTGCAATGAGAGCTATTCAATTTTATGAACATAAGCTGATATCCGGGCA 286
QY 241 GACGCCAGATCGCTGTTGTTGAAGGCCACCAAGATCTGCGTGAATGGCAAAAACAATG 300
DB 287 GATGCCAGTATCGATGTTGTTGAAGGCCACCAAGATCTGTTGAAGGCCAAGAGCAGAAG 346
QY 301 AATTCTACAGCTGTGTGAGTGAACATAACAGAGGCTTCCAAAGCCAGACCAAGCT 360
DB 347 CAGACCTACAGCTGTGTGAGTGAACATAACAGAGGCTTCCAGACTCAGACCAAGCCT 406
QY 361 TCCGGCGGCAATGACATCTCTATGTAGGCTCCCTGTGAGCTGAGCACTCTAT 420
DB 407 TCTGGCGGCAATGAGATGTTTCTTACGTAGGCTTTCAGTGAAGCTGAATACAGCTAT 466
QY 421 CTGATAGGCGCCATAACATCCCAATGTATATATGAATGAGAGACCCCTTCTTGTCT 480
DB 467 TTCAATGAGAGCCATATATATCCCAATGAAATATGAAGAGATGAGCCCTCTCTGTGCT 526
QY 481 GTGAATTCACCTCGCAGAGGTGC 504
DB 527 GTGAATTCACCTCGCAGAGGTGC 550

Search completed: May 28, 2003, 10:13:50
Job time : 3619.13 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:34:39 ; Search time 290.439 Seconds
(without alignments)
11770.723 Million cell updates/sec

Title: US-09-778-971-4

Perfect score: 2589

Sequence: 1 gtggccagtgccggcgccat.....aaaaaaaaaaaaaaaaaa 2589

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 828747 seqs, 66023138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1472.2	56.9	1563	10	US-09-778-971-3
3	644.8	24.9	1796	9	US-09-863-818A-1
4	643.2	24.8	1827	10	US-09-778-971-1
5	643.2	24.8	1841	10	US-09-886-404-17
6	643.2	24.8	2015	10	US-09-886-404-19
7	632.2	24.4	637	9	US-09-863-818A-3
8	625.6	24.2	1515	9	US-09-874-503-11
9	625.6	24.2	1515	9	US-10-000-157-11
10	625.6	24.2	1515	9	US-10-063-547-157
11	625.6	24.2	1515	9	US-09-747-259-11
12	625.6	24.2	1515	9	US-10-174-590-399
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					Sequence 399, App

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22	625.6	24.2	1515	9	US-10-176-913-399	Sequence 399, App
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ALIGNMENTS

RESULT 1
US-09-778-971-4
Sequence 4, Application US/09778971
Patent No. US20020102639A1
GENERAL INFORMATION:
APPLICANT: Shaughnessy, John D.
TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
FILE REFERENCE: D6138
CURRENT APPLICATION NUMBER: US/09/778, 971
PRIOR APPLICATION NUMBER: US 60/180, 374
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 2589
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: prim transcript
OTHER INFORMATION: cDNA of mouse Evi27
US-09-778-971-4

Query Match	100.0%	Score 2589;	DB 10;	Length 2589;
Best Local Similarity	100.0%	Pred. No. 0;		
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DB	121	ATGTGTCACACACTCACTCCAGAGACTTGAGGAGCCTCCAGTGAAGTCTGCAAG	180	
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Db	1441	TGCTTTGCTCAGAGACAAAGTGTCCCATCCCTCCAGATACAAACAAGACGATGCTGGAG	1500
Qy	1501	GCTGGCTGCCCTCTTCTCCTGTGCTGCTGGTGGCTGTGGGTGCTGGACGCTGGAGTCT	1560
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Qy	1561	ACCTAACCTTGGAGGCAAGAGAGACGAGACGTCCTTTCTATATTTCCACACATGCTCC	1620
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Qy	1681	GTGCGTTCACCTGACCTTCTCTTCAAAACCTACGACGAGAGTGAAGTCACTCTGAAAAATGAGC	1740
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Db	1741	AGAAAAAGAAAAATGCGCCGAGATGAGGCGCGGTACAGTGCTGACCACTGAGAAACAAAGCGG	1800
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Qy	1861	GGCAACAATGAGGAGGAGCGCCAGGGAGAACTCTCAGAGATCTGTTCCTCTGCGCTTTAAC	1920
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Qy	2041	TGAAGACGCGCACAGCTTCCACACAGAACTTCTAAGGCTACGAGACAGATGTCAGTGA	2100
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Qy	2101	AGAAACCTCACAAGGCTGTGCATGATAGCTGTTCACCTTGTAGTCCACCCGCGGGGAATA	2160
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Db 2461 GCTGTCTGACAGTTGGGTCTGTCTTGCATCTGCCATGCTATATGCTGACAGTAGACCGT 2520
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Qy 2581 AAAAAAAAAA 2589
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RESULT 2

US-09-778-971-3
; Sequence 3, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: prim.transcript
; OTHER INFORMATION: cDNA of mouse Evi27
US-09-778-971-3

Query Match 56.9%; Score 1472.2; DB 10; Length 1963;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 607 AATTTCACAACCAATCCCTTGGAAAAGATACAGATTCTCATTCAGGACAGACA 666
Qy 1293 TTGGGGTTTTCTAGAGTGTGAGAAATAAATGATGAGAGAGTGTGAGCATCCGGTG 1352
Db 667 TTGGGGTTTTCTAGAGTGTGAGAAATAAATGATGAGAGAGTGTGAGCATCCGGTG 726
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Db 787 GACTGCATCCGACGCGAAGGACAGTGTGCTTGGCTCAGAGACAAGTGTCCCATCCCT 846
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Qy 1893 CAGATCTGTCCCTCTTGAACCTTGTGATGATTTGACAGCAGACGAT 1952
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Qy 1953 CTGACAAATACCTGTGTATCTTGGGAGACAGACCTCAAGGCGACTAATATGCC 2012
Db 1327 CTGACAAATACCTGTGTATCTTGGGAGACAGACCTCAAGGCGACTAATATGCC 1386
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Qy 2433 ATGAAGTATATAGGACCTTCCCTGAGGCTGTCTGTCAGTGTGGTGTCTGTGACTG 2492
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Qy 2493 CCCATGCTATGCTGACAGTGAAGCGTTTGTAACTTTATCTGTATGAATATC 2552
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Qy 2553 CGTTTGGGAGCTCTCAAAAAAAAAAAAAAAAAA 2589
Db 1927 CGTTTGGGAGCTCTCAAAAAAAAAAAAAAAAAA 1963

RESULT 3

US-09-863-818A-1
; Sequence 1, Application US/09863818A
; Publication No. US20030092881A1

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; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DKO170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1509)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (46)..()
; OTHER INFORMATION:
US-09-863-818A-1

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Query Match      24.9%; Score 644.8; DB 9; Length 1796;
Best Local Similarity 76.0%; Pred. No. 6.6e-200;
Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;

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DB 472 TTTCATTCCAGGCTGCTTAACACGATATGAATTAATAAGCATGACGAGCG 531
QY 1173 GGAAGCTGTGGGACCGAGACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGTG 1232
DB 532 GGAAGCTGTGGGATCCGAAACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGTG 591
QY 1233 AATTTCACAACCATTCCTCTTGGAAACAGATACAGATTCTCATTCACGGGACAGACA 1292
DB 592 AACTTCACAACCATTCCTCTTGGAAACAGATACAGATTCTCATTCACAGCACTATC 651
QY 1293 TTGGGGTTTCTAGAGTCTGG-----AGATAAATCATGATGAGAGAGCTGTAGGCC 1343
DB 652 ATCGGGTTTCTAGAGTCTGG-----AGATAAATCATGATGAGAGAGCTGTAGGCC 711
QY 1344 ATCCCGGTGACTGAGAGAGTGAAGTGCCTGTGCTGAGTGAACCCATATTTACATACC 1403
DB 712 ATTCAGTGAAGTGGGATGATGAGAGTGTACGCTGAGTGAACCCATATTTCTACT 771
QY 1404 TCGGGCATGATCTGATCCGACGCGAAAGGACAGTTGCTTGTCTCAAGACAGAGTCT 1463
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QY 1464 CCATATCCCTCCAGATGACAGACAGACGATGCTGGAGGCTGGCTGCTCTTCTCTG 1523
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DB 892 TCTGTGCTGTGTGGGCTGCTGAGCTGGATCTTAACCTTAAGGACAGGA 951
QY 1581 AGGAGCAGGAAGAGCTCTTCTTAATTTCCACCAATGCTCTGCTCCCTCATTAAGTCTG 1640
DB 952 AGGATCAAGAGAGCTCTTCTTAATTTCCACCAATGCTCTGCTCCCTCATTAAGTCTG 1008
QY 1641 GTGGTTATCTCTGTGATATGTTTCATATCAACCGCTGTGCTCTCACTGACTTTCTT 1700
DB 1009 GTGGTTATCTCTGTGATATGTTTCATATCAACCAATGTTGTTCACTGAAATTTCTT 1068
QY 1701 CAAATCTACTGACAGAGTGAAGTCTCTTGAATAATGAGAGAAATGAGCGAG 1760
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DB 1129 ATGGTCCAGTGCAGTGGCTTGCCACTCAAAAGAGAGACAGACAAAGTGTCTTCTT 1188
QY 1821 CTTCCAGTGCAGTGGCTTGCCACTCAAAAGAGAGACAGACAAAGTGTCTTCTTCTT 1880
DB 1189 CTTCCAGTGCAGTGGCTTGCCACTCAAAAGAGAGACAGACAAAGTGTCTTCTTCTT 1248
QY 1881 AGGAGAGTCTGAGATCTGTTCCCTTGGCTTGAACCTCTTTTGTAGATTTCAAC 1940
DB 1249 AGTGAAGTCTCAAGAGCTCTTCCCTTGGCTTGAACCTCTTTTGTAGATTTCAAG 1308
QY 1941 AGCCAGAGCATCTGACAAATATCTGTGTGTATCTTGGGGAGACAGACCTCAAGGC 2000
DB 1309 AGCCAGATCTGACAAATATCTGTGTGTATCTTGAAGATTAATCAAAAGAC 1368
QY 2001 GACTATATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2060
DB 1369 GATTACATGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
QY 2061 CACAGAACTTCTCAAGCTACGAGACATGTCAGTGAAGAAACCTTCAAGCTGCTC 2120
DB 1429 TGTGAGAACTTCTCAAGCTACGAGACATGTCAGTGAAGAAACCTTCAAGCTGCTC 1488
QY 2121 CATGATGCTGTTCAACCTTGTATGTCACCCGGGGAA--TAGACCTTGAAGCTTTC 2178
DB 1489 CACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
QY 2179 TACTCTCCCTTCAGTGAAGAAATGCTGTGTCAGTCTGGA 2220
DB 1549 TATCCACCAATTAACGAGAAACAGTGTGATGATCTGGA 1590

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RESULT 4
US-09-778-971-1
; Sequence 1, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Ev127 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: prim_transcript
; OTHER INFORMATION: cDNA of human Ev127
US-09-778-971-1

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Query Match      24.8%; Score 643.2; DB 10; Length 1827;
Best Local Similarity 75.9%; Pred. No. 2.2e-199;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

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DB 474 TTTCATTCCAGGCTGCTTAACACGATATGAATTAATAAGCATGACGAGCG 533
QY 1173 GGAAGCTGTGGGACCGAGACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGTG 1232
DB 534 GGAAGCTGTGGGATCCGAAACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGTG 593
QY 1233 AATTTCACAACCATTCCTCTTGGAAACAGATACAGATTCTCATTCACGGGACAGACA 1292
DB 594 AACTTCACAACCATTCCTCTTGGAAACAGATACAGATTCTCATTCACAGACTATC 653
QY 1293 TTGGGGTTTCTAGAGTCTGG-----AGATAAATCATGATGAGAGAGCTGTAGGCC 1343
DB 654 ATCGGGTTTCTAGAGTCTGG-----AGATAAATCATGATGAGAGAGAGCTGTAGGCC 713

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QY 1344 ATCCGGTACTGAGAGAGTAAAGTGGGTGTTGAGTGAACCCCATTTTACATACC 1403
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QY 1524 ---CTGCTGTGGTGTGTGTGGTGTGGAGCTGGAGTCTAACTTGAAGGACGAA 1580
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QY 1581 AGGAGACGAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1640
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Db 1011 GTGTTTATCCCATCTGAATATGTTTTCATACACAAATTTTACTTCACTGAAATTTCT 1070
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QY 1761 ATGGGGCCGGTACAGTGGTGAACACTCAGAAAGCGGAGATTAATGTGCTTCTT 1820
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Db 1131 ATGGGGTCAAGTGAAGTGGTGTGCACTCAAAAGAGAGAGAGCAAGTGTCTTCTT 1190
QY 1821 CTTCAGTGAAGTCCGACCTTTGTGACAGTGGTGGCCAGTGAAGGAGGAGCGC 1880
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; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/866,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1555)
; US-09-866-404-17

Query Match          24.8%; Score 643.2; DB 10; Length 1841;
Best Local Similarity 75.9%; Pred. No. 2.2e-199;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

QY 1113 TTCACATTCAGAGCTGCTTAACCAAGTAAATATTAAGAGTCACTGAGGCG 1172
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QY 1173 GGAAGCTGTGGAGCCGACATCACTGTTTGAAGAAAGAGAAAGTGTGAAGT 1232
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QY 1233 AATTTCACAAACCAATCCCTTTGAAACAGATACAGATCTCATTTCAAGGAGACAGACA 1292
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QY 1293 TTGGGGTTTCTAGAGTGTG-----AGAAATACTGATGAGAGAGCTGTAGCC 1343
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QY 1344 ATCCGGTACTGAGAGAGTAAAGTGTGGTTCAGCTGAACCCATATTTACATACC 1403
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Db 818 TGTGGAGGAGTGTGATCCGATTAAGAGAGAGTGTGCTTGTGCTCAGAGCAAGTGTCT 877
QY 1464 CCCATCCCTTCAGATGACAAACAGAGCATGTGGAGGCTGCTCTCTTCTGTGTG 1523
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QY 1761 ATGGGGCCGGTACAGTGGTGAACACTCAGAAAGAGGCGAGATTAAGTGTCTTCTT 1820
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QY 1821 CTTCAGTGAAGTCCGAGACCTTTGTGACAGTGTGTGGCCAGATGAGGAGCGCC 1880

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RESULT 5
US-09-866-404-17

; Sequence 17, Application US/09866404
; Patent No. US2002003752A1

; GENERAL INFORMATION:

; APPLICANT: Medlock, Eugene

; APPLICANT: Yeh, Richard

; APPLICANT: Silbiger, Scott M.

; APPLICANT: Elliott, Gary S.

; APPLICANT: Nguyen, Hung Q.

; APPLICANT: Jimg, Shuglian

; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof


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? APPLICANT: Gorman, Daniel M.
? TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
? FILE REFERENCE: DKO1170K
? CURRENT APPLICATION NUMBER: US/09/863,818A
? CURRENT FILING DATE: 2001-05-23
? PRIOR APPLICATION NUMBER: US 60/206,862
? PRIOR FILING DATE: 2000-05-24
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3
? LENGTH: 637
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(210)
? OTHER INFORMATION:
? US-09-863-818A-3

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1 APPLICANT: Chen, Jian
2 APPLICANT: Filvaroff, Ellen
3 APPLICANT: Fong, Sherman
4 APPLICANT: Goddard, Audrey
5 APPLICANT: Godowski, Paul J.
6 APPLICANT: Grimaldi, J. Christopher
7 APPLICANT: Gurney, Austin L.
8 APPLICANT: Li, Hanzhong
9 APPLICANT: Hillan, Kenneth J.
10 APPLICANT: Hymowitz, Sarah G.
11 APPLICANT: Tumas, Daniel
12 APPLICANT: Starovassnik, Melissa A.
13 APPLICANT: Vanlookeren, Menno
14 APPLICANT: Vandlen, Richard
15 APPLICANT: Watanabe, Colin K.
16 APPLICANT: Williams, P. Mickey
17 APPLICANT: Wood, William I.
18 APPLICANT: Yansura, Daniel
19 TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
20 FILE REFERENCE: P1381R1C1P3 (US)
21 CURRENT FILING DATE: 2001-06-05
22 CURRENT FILING NUMBER: US/09/874,503
23 PRIOR FILING DATE: 2000-11-28
24 PRIOR FILING NUMBER: US 60/253,646
25 PRIOR APPLICATION NUMBER: US 60/242,837
26 PRIOR FILING DATE: 2000-10-24
27 PRIOR FILING NUMBER: US 60/175,481
28 PRIOR FILING DATE: 2000-01-11
29 PRIOR APPLICATION NUMBER: US 60/191,007
30 PRIOR FILING DATE: 1999-12-23
31 PRIOR APPLICATION NUMBER: US 60/138,387
32 PRIOR FILING DATE: 2000-06-22
33 PRIOR APPLICATION NUMBER: US 60/172,096
34 PRIOR FILING DATE: 1999-12-23
35 PRIOR APPLICATION NUMBER: US 60/130,232
36 PRIOR FILING DATE: 1999-04-21
37 PRIOR APPLICATION NUMBER: US 60/113,621
38 PRIOR FILING DATE: 1998-12-23
39 PRIOR APPLICATION NUMBER: US 60/085,579
40 PRIOR FILING DATE: 1998-05-15
41 PRIOR APPLICATION NUMBER: US 09/854,208
42 PRIOR FILING DATE: 2001-05-10
43 PRIOR APPLICATION NUMBER: US 09/854,280
44 PRIOR FILING DATE: 2001-05-20
45 PRIOR APPLICATION NUMBER: US 09/816,744
46 PRIOR FILING DATE: 2001-03-22
47 PRIOR APPLICATION NUMBER: US 09/747,259
48 PRIOR FILING DATE: 2000-12-20
49 PRIOR APPLICATION NUMBER: US 09/644,848
50 PRIOR FILING DATE: 2000-08-22
51 PRIOR APPLICATION NUMBER: US 09/380,142
52 PRIOR FILING DATE: 1999-08-25
53 PRIOR APPLICATION NUMBER: US 09/380,138
54 PRIOR FILING DATE: 1999-08-25
55 PRIOR APPLICATION NUMBER: US 09/311,832
56 PRIOR FILING DATE: 1999-05-14
57 PRIOR APPLICATION NUMBER: US PCT/US01/06520
58 PRIOR FILING DATE: 2001-02-28
59 PRIOR APPLICATION NUMBER: US PCT/US00/34956
60 PRIOR FILING DATE: 2000-12-20
61 PRIOR APPLICATION NUMBER: US PCT/US00/32678
62 PRIOR FILING DATE: 2000-12-01
63 PRIOR APPLICATION NUMBER: US PCT/US00/30873
64 PRIOR FILING DATE: 2000-11-10
65 PRIOR APPLICATION NUMBER: US PCT/US00/23328

PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 11
LENGTH: 1515
TYPE: DNA
ORGANISM: Homo Sapien
US-09-874-503-11

Query Match 24.2%; Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1.1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

QY 1113 TTTCATTCCAGGCTGCTTAACAGCTATGTAATTAATAAGAGCTGACGAGGCG 1172
DB 475 TTTCCTCACCAGGCTGCTTAACAGCTATGTAATTAATAAGAGCTGACGAGGCG 534
QY 1173 GGAAGCTGCGGAGTCCGAACTATGCTTTGTAAGAGAGAGAGAGAGAGAGAG 1232
DB 535 GGAAGCTGCGGAGTCCGAACTATGCTTTGTAAGAGAGAGAGAGAGAGAGAG 594
QY 1233 AATTTCACAACTATGCTTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
DB 595 AATTTCACAACTATGCTTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 654
QY 1293 TTGGGGTCTTCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1343
DB 655 ATGCGGTTTCTCAGGTTTGAAGCCACACAGAGAGAGAGAGAGAGAGAGAGAG 714
QY 1344 ATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403
DB 715 ATTCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 774
QY 1404 TGGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1463
DB 775 TGGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
QY 1464 CCATCCCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1523
DB 835 CTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
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DB 895 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
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DB 955 AGGAGCGAG 1011
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QY 1701 CAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
DB 1072 CAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
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DB 1132 ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
QY 1821 CTTCCAGTGAAGTCCGAG 1880
DB 1192 CTTCCAGTGAAGTCCGAG 1251
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DB 1252 AGGAG 1311
QY 1941 AGGAG 2000
DB 1312 AGGAG 1371
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DB 1372 GACTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431
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RESULT 9
US-10-000-157-11
Sequence 11, Application US/10000157
Publication No. US20020182673A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah
APPLICANT: Tumas, Daniel
APPLICANT: Starovasnik, Melissa.
APPLICANT: Vanhookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Matanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Yansura, Daniel
FILE REFERENCE: P1381C1P4 (US)
CURRENT APPLICATION NUMBER: US/10/000.157
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/172096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21

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PRIOR APPLICATION NUMBER: 60/213807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/242837
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PRIOR FILING DATE: 2001-08-13
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PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 11
LENGTH: 1515
TYPE: DNA
ORGANISM: Homo Sapien

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US-10-000-157-11
Query Match      24.2%; Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1.1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

QY 1113 TTTCACATTCCTCCAGGCTGCTTAAACCAAGTAATGTAATATTAAGAGAGTCACTGAGCG 1172
DB 475 TTCACTTCAACGAGGCTGCTTAAACCAAGTAATGTAATATTAAGAGAGTCACTGAGCG 534
QY 1173 GGAAGCTGTGGAGCCCAACATCACTGCTTAAAGAAAGAGAGAGTGTGAGTG 1232
DB 535 GGAAGCTGTGGAGCCCAACATCACTGCTTAAAGAAAGAGAGAGTGTGAGTG 594
QY 1233 AATTTTCAACAACCAATCCCTTGAAGACAGATACAGATTCATTAACAGGACACAGCA 1292
DB 595 AACTTCAACAACCAATCCCTTGAAGACAGATACAGATTCATTAACAGGACCTATC 654
QY 1293 TTGGGGTTTCTAGAGTGTG-----AGATTAACATGATGAGAGCTGTAGCC 1343
DB 655 ATCGGGTTTCTCAGGTGTTTGAAGCCACACAGAGAAACAAACGAGACTTCAGTGTG 714
QY 1344 ATCCCGTGAATGAGAGAGTGAAGTGGGTGCTTCACTGACCCATATTACATACC 1403
DB 715 ATTCAGTGAATGAGAGAGTGAAGTGGGTGCTTCACTGACCCATATTACATACC 774
QY 1404 TCGGCAATGATGATCGATCCGACGGAAGGACAGTTGTCTTGTCTCAGAGCAAGTGCT 1463
DB 775 TTGGCAGGAGATCGATCCGACGGAAGGACAGTTGTGTCTTGTCTCAGAGCAAGTGCT 834
QY 1464 CCATTCCTTCGATGATGACAAACAGACGATCTGGAGAGCTGCTGCTTCTCTGTG 1523
DB 835 CTTTCCCTTCGATGATGACAAACAGACGATCTGGAGAGCTGCTGCTTCTCTGTG 894
QY 1524 ---CTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1580
DB 895 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 954
QY 1581 AGGACAGCAAGACGCTCTTCTTATTTCCACATGCTCTCTCTCTCTCTCTCTCTCTCT 1640
DB 955 AGGATCAAGAAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1011
QY 1641 GTGTTTATCTCTTCTGAGATATGTTTCAATCAACCGTCTGTGCTTCACTGATCTTCT 1700
DB 1012 GTGTTTATCTCTTCTGAGATATGTTTCAATCAACCGTCTGTGCTTCACTGATCTTCT 1071
QY 1701 CAAAATCTGCAAGAGTGAAGTCTCTTGAAGAAATGSCAGAAAGAAATGSCAGAG 1760
DB 1072 CAAAATCTGCAAGAGTGAAGTCTCTTGAAGAAATGSCAGAAAGAAATGSCAGAG 1131
QY 1761 ATGGGGCGGTACAGTGTGCTGCACTGAGAGCAAGGCGAGATTAAGTGTCTCTCT 1820
DB 1132 ATGGGGCGGTACAGTGTGCTGCACTGAGAGCAAGGCGAGATTAAGTGTCTCTCT 1191
QY 1821 CTTCCAGTGAAGTCCCGACCTTTGTGACAGTGTGCTGSCACAAATGAGGAGAGCGCC 1880
DB 1192 CTTCCAGTGAAGTCCCGACCTTTGTGACAGTGTGCTGSCACAAATGAGGAGAGCGCC 1251
QY 1881 AGGAGAACTCTCAGAGTGTGCTTCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1940
DB 1252 AGTGAAGAACTCTCAGAGTGTGCTTCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1311
QY 1941 AGCCAGAGCATCTGCAACAAATACGAGTGTGCTTCTTGTGAGAGATTTGATCAAGAGC 2000
DB 1312 AGCCAGATTCATCTGCAACAAATACGAGTGTGCTTCTTGTGAGAGATTTGATCAAGAGC 1371
QY 2001 GACTTAATGCTCTGAGTGTGCTGCCCCCAATATCACTCATAGAGAGCGCACAGCTTTC 2060
DB 1372 GATTAATGCTCTGAGTGTGCTGCCCCCAATATCACTCATAGAGAGCGCACAGCTTTC 1431
QY 2061 CACACAGAACTTCTCAGAGCTTACGAGAGCATGTCAGTGAAGAAAGCTCAGACAGCTTGC 2120
DB 1432 TGTGAGAACTTCTCAGATGTCAAGCAGAGGTGTGAGCAGAGAAAGATCAAGAGCTTGC 1491

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QY 1821 CTTCCAGTACGTCCCGACCCCTTGTGACAGTGCCTGTGGCCCAATGAGGGCAGCGCC 1880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1192 CTTTCCAAATGAGGTAAAGTGTGTGCGATGTAACCTGTGGCAAGGCGAAGCTCC 1251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1881 AGGGAATCTTCAGAGATCTGTCTTCCCTTTGCTTTAACTCTTTTGTATGATTTTACG 1940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1252 AGTGAATCTTCAGAGATCTGTCTTCCCTTTGCTTTAACTCTTTTGTATGATTTTACG 1311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1941 AGCCAGAGCATCTGCAGAAATACCTGTGTATCTTGTGGGGAGACAGACCTCAAGGC 2000
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1312 AGCCAGATTCATCTGCAGAAATACCTGTGTATCTTGTGTATGAGATTTATCAAAAGAC 1371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2001 GACTTAATGCTGCTGAGTGTCTGCCCCCAATATCATCTCATGAGAGCCCAAGCTTTC 2060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1372 GATTCAATGCTGTGAGTGTCTGCCCCCAAGTACCACTCATGAGAGATGCACTGCTTTC 1431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2061 CACACAGAACTTCTCAGAGCTACGAGAGCATCTCATGTAGAAACGCTCACAGCTTGC 2120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1432 TGTGCAAGACTTCTCATGTCTCAAGCAGAGTGTCTCAGCAGAAAAAGATCACAGCTGC 1491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2121 CATGATAGCTGTTCACCTTTGAG 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1492 CACGATGCTGTCTGCTTTGAG 1515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 14

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US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Balton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157

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Query Match      24.2% Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1.1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

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QY 1113 TTCACTTCCAGGCTGCTTAACCAAGTAATGAAATATTAAGAGAGTCACTGAGGCG 1172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 TTCACTTCCAGGCTGCTTAACCAAGTAATGAAATATTAAGAGAGTCACTGAGGCG 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1173 GGAAGGCTGTGGGACCCAGACATCACTGCTTGTAAAGAGAGAGAGATGGTGAAGTG 1232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 GGAAGGCTGTGGGATCGAATCATCACTGCTTGTAAAGAGAGAGAGATGGTGAAGTG 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1233 AATTTCACAAACCAATCCCTTGTGAAACAGATACAGATTTCTCATTTCAAGCGGACAGACA 1292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 AACTTCACAAACCACTCCCTGTGGAAACAGATACATGCTTTATTCACACAGCACTATTC 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1293 TTGGGGTTTCTAGAGTGTCTG-----AGATTAATCTGATGAGAGCTGTGAGCC 1343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 ATCGGGTTTCTAGAGTGTGAGCCACACAGAGAAACAAACGAGACTTCATGAGTG 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 1344 ATCCGGTACTGAGAGAGATGAGGTGGGTGTTCACTGACCCCATATTTTACATACC 1403
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DB 745 ATTCCAGTACTGAGGAGATGATGAGAGTGTCTACGTGACACTGATCATATTTTCTACT 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1404 TCGGCAATGATCTGATCCGAGCGGAGGAGACATTTGTCTTTGCTCAGAGACATGTCT 1463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 TGTGCAAGGATCTGATCCGATTAAGAGACATTTGTCTTTGCTCAGAGACATGTCT 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1464 CCCATCCCTCCAGATGACAAACAGACATCTGGGAGGTGGCTGCTCTCTTCCGGTG 1523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 CTTTTCCTCTGATTAACAAACAAAGACCGGAGAGGTGGCTGCTCTCTCTGCTG 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1524 ---CTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 954
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1581 AGGAGCAGAAACGTCCTTTCTATTTTCACATGCTCTGCTCTCTATTAAGTCTCG 1640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 955 AGGATCAAGAAACCTCTCTTTCTA---CCACCAACATCTGCCCCCATTAAGTCTT 1011
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1641 GTGTTTATCTTCTGAGATATGTTTCAATCAACCGTGTGTGTGTGTGTGTGTGTGTGT 1700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1012 GTGTTTATCTTCTGAGATATGTTTCAATCAACCGTGTGTGTGTGTGTGTGTGTGTGT 1071
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1701 CAAACTACTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1072 CAAACATGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1761 ATGGGCGGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1820
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1132 ATGGGCTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1821 CTTCCAGTACGTCCCGACCCCTTGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1192 CTTTCCAAATGAGGTAAAGTGTGTGCGATGTAACCTGTGGCAAGGCGAAGCTCC 1251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1881 AGGGAATCTTCAGAGATCTGTCTTCCCTTTGCTTTAACTCTTTTGTATGATTTTACG 1940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1252 AGTGAATCTTCAGAGATCTGTCTTCCCTTTGCTTTAACTCTTTTGTATGATTTTACG 1311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1941 AGCCAGAGCATCTGCAGAAATACCTGTGTATCTTGTGTGTGTGTGTGTGTGTGTGT 2000
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1312 AGCCAGATTCATCTGCAGAAATACCTGTGTATCTTGTGTGTGTGTGTGTGTGTGTGT 1371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2001 GACTTAATGCTGCTGAGTGTCTGCCCCCAATATCATCTCATGAGAGCCCAAGCTTTC 2060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1372 GATTCAATGCTGTGAGTGTCTGCCCCCAAGTACCACTCATGAGAGATGCACTGCTTTC 1431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2061 CACACAGAACTTCTCAGAGCTACGAGAGCATCTCATGTAGAAACGCTCACAGCTTGC 2120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1432 TGTGCAAGACTTCTCATGTCTCAAGCAGAGTGTCTCAGCAGAAAAAGATCACAGCTGC 1491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 2121 CATGATAGCTGTTCACCTTTGAG 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1492 CACGATGCTGTCTGCTTTGAG 1515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 15

```

US-10-175-737-399
; Sequence 399, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175, 737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-399

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Query Match      24.2%; Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1,1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

```

```

QY 1113 TTTCATATCCAGGCTGCTTAACCGATATGAAATATTAAGAGCTGCACTGAGCGC 1172
DB 475 TTTCATCCACCGAGGCTGCTTAACCGATATGAAATATTAAGAGGCTGTCAGGCC 534
QY 1173 GGAAGCCTGTGGAGCCGAGACATGCTGCTTAAGAAAGAGAGATGTTGAAGTG 1232
DB 535 GGAAGCCTGTGGAGCTGCGAATCATCTGTTGAGAGAGAGAGAGAGAGAGAGAG 594
QY 1233 AATTTCACAACCAATCCCTTGGAAACAGATACAGATTCTCAATCAACGGGACAGCA 1292
DB 595 AACTTCACAACCACTCCCTGGGAAACAGATACAGATTCTTATCAACAGACATATC 654
QY 1293 TTGGGGTTTCTAGAGTCGTG-----AGATTAAGTGAAGAGAGTCTGTAGCC 1343
DB 655 ATCGGGTTTCTAGAGTTTGAAGCCACACGAGAAACAAAGCGAGCTTCAAGTGTG 714
QY 1344 ATCCCGGTGACTGAGAGAGTGAAGTGCAGTGTTCAGCTGACCCCATATTTACATACC 1403
DB 715 ATTCCAGTACTGGGAGATGAGAGAGTGTACAGTGTGACCTGACCTATTTTCTACT 774
QY 1404 TCGGGCAATGACTGATCCGACGCGAAGGAGACAGTTGTGCTTGTCTAGAGACAGTGT 1463
DB 775 TGTGGCAGCGACTGATCCGACATTAAGAAAGAGTGTGCTGTGCCAACAAGCGGTC 834
QY 1464 CCCATCCCTCCCAATGACCAAGACGATGCTGGAGAGGCTGCTGCTCTTCTGTGTG 1523
DB 835 CTTTCCCTCTGATTAACAAAGAAAGACCGGAGGCTGCTGCTCTCTCTGCTG 894
QY 1524 ---CTGCTGTGCTGTGTGGGTGCTGGAGCTGGAGTCTACCTTAAGAGGAGGA 1580
DB 895 TCTCTGTGTGTGGCAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 954
QY 1581 AGGAGCAGAAAGCTCTTCTTCTATTTCACCAATGCTCTGCCCCCATTAAGTCTG 1640
DB 955 AGGATCAAGAAAGCTCTTCTTCTA---CCACCACTACTGCCCCCATTAAGTCTT 1011
QY 1641 GTGTTTATCTCTGTGATATGTTTCCATCAACCGTGTGTGCTTCACTGACTTCTT 1700
DB 1012 GTGTTTATCCCATCTGAAATATGTTTCCATCAACCAATTTGTTACTGAAATTTCTT 1071
QY 1701 CAAACTACTGCAAGAGTGAAGTCACTCTTGAAGAAATGGCAAGAAATGCGCGAG 1760
DB 1072 CAATCACTGCAAGAGTGAAGTCACTCTTGAAGAAATGGCAAGAAATGCGAG 1131
QY 1761 ATGGGGCGGGTACAGTGTGACCTCAGAGCAAGCGGCAAGTAAAGTGTCTTCTT 1820
DB 1132 ATGGGTTCAGTGAAGTGTGCTTGCACAAAGAGGACAGACAAAGTGTCTTCTT 1191
QY 1821 CTTCCCAATGACGTCGAGACCTTTTGTGACAGTGTGTGCGCAATGAGGAGCGCC 1880
DB 1192 CTTTCAATGACGTCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1251
QY 1881 AGGAGAACTCTGAGAGTGTGCTTCTGCTTAACTCTTTGTAGATTTCAAG 1940
DB 1252 AGTGAATCTCTCAAGACTCTTCTGCTTCTTAACTCTTGTGAGTGAATTAAGA 1311

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QY 1941 AGCCAGACGATGTGACAAATACCTGTGTGTCTATCTTGGGGAGACACTCAAGGC 2000
DB 1312 AGCCAGATCTCTGCAAAATACGTGTGTCTACTTTAGAGATGATGACAAAGAG 1371
QY 2001 GACTATTAATGCCCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2060
DB 1372 GATTACAAATGCTCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1431
QY 2061 CACACAACTTCTCAAGGCTACGACAGACATGTCAAGTGAAGAAAGCTCACAGCTTC 2120
DB 1432 TGTGCAAGATCTTCTCATGTCAAGACAGAGTGTCAAGAGAAAGATCACAGCTTC 1491
QY 2121 CATGATAGCTGTTCACCTTTGAG 2144
DB 1492 CACGATGCTGTGTCTCTTGTAG 1515

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:31:59 ; Search time 86.0664 Seconds
(without alignments)
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Title: US-09-778-971-4

Perfect score: 2589
Sequence: 1 GFGGCGAGTGGCGGCGCAT.....aaaaaaaaaaaaaaaaa 2589

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46.6	1.8	259	US-08-222-177A-24	Sequence 24, Appl
C 2	45.2	1.7	7218	US-08-232-463-14	Sequence 14, Appl
C 3	44.4	1.7	6953	US-07-805-123C-2	Sequence 2, Appl
C 4	44.4	1.7	6953	US-08-033-081B-2	Sequence 2, Appl
C 5	44.2	1.7	62	US-08-222-177A-56	Sequence 56, Appl
C 6	43.8	1.7	22846	US-08-469-461-3	Sequence 3, Appl
C 7	43.8	1.7	22846	US-07-890-609-3	Sequence 3, Appl
C 8	42	1.6	2529	US-09-051-969A-5	Sequence 5, Appl
C 9	41.2	1.6	2997	US-08-486-343A-3	Sequence 3, Appl
C 10	41.2	1.6	2997	PCT-US95-07349-3	Sequence 3, Appl
C 11	41.1	1.6	50	US-08-222-177A-169	Sequence 169, App
C 12	40.8	1.6	3854	US-08-720-484A-1	Sequence 1, Appl
C 13	40.8	1.6	3854	US-08-953-823A-1	Sequence 1, Appl
C 14	40.8	1.6	3854	US-09-398-239-1	Sequence 1, Appl
C 15	40.4	1.6	2360	US-08-916-043-3	Sequence 3, Appl
C 16	40.2	1.6	210	US-08-222-177A-23	Sequence 23, Appl
C 17	40	1.5	1083	US-09-177-650-121	Sequence 121, App
C 18	39.6	1.5	155	US-08-222-177A-19	Sequence 19, Appl
C 19	39.4	1.5	818	US-08-205-697A-4	Sequence 4, Appl
C 20	39.4	1.5	818	US-08-702-525-4	Sequence 4, Appl
C 21	39.4	1.5	818	PCT-US95-02576-4	Sequence 4, Appl
C 22	39.4	1.5	1570	US-08-205-697A-10	Sequence 10, Appl
C 23	39.4	1.5	1570	US-08-702-525-10	Sequence 10, Appl
C 24	39.4	1.5	1570	PCT-US95-02576-10	Sequence 10, Appl
C 25	39.4	1.5	1606	US-08-702-525-64	Sequence 64, Appl
C 26	39.4	1.5	1606	US-08-702-525-64	Sequence 64, Appl
C 27	39.4	1.5	1888	PCT-US95-02576-64	Sequence 64, Appl
C 27	39.4	1.5	1888	US-08-205-697A-1	Sequence 1, Appl

C 28	39.4	1.5	1888	US-08-702-525-1	Sequence 1, Appl
C 29	39.4	1.5	1888	PCT-US95-02576-1	Sequence 1, Appl
C 30	39.4	1.5	2516	US-08-205-697A-3	Sequence 3, Appl
C 31	39.4	1.5	2516	US-08-702-525-3	Sequence 3, Appl
C 32	39.4	1.5	2516	PCT-US95-02576-3	Sequence 3, Appl
C 33	39.2	1.5	190	US-08-222-177A-13	Sequence 13, Appl
C 34	39.2	1.5	1920	US-09-534-638-6	Sequence 6, Appl
C 35	39.2	1.5	9840	US-09-534-638-1	Sequence 1, Appl
C 36	39.2	1.5	11970	US-09-345-217-1	Sequence 1, Appl
C 37	39.2	1.5	152331	US-09-128-155-16	Sequence 16, Appl
C 38	39	1.5	2791	US-09-570-367C-1	Sequence 1, Appl
C 39	38.8	1.5	42	US-08-455-627-22	Sequence 22, Appl
C 40	38.8	1.5	42	US-08-689-856-22	Sequence 22, Appl
C 41	38.8	1.5	35100	US-08-306-691B-19	Sequence 19, Appl
C 42	38.8	1.5	35100	PCT-US93-06251-19	Sequence 19, Appl
C 43	38.8	1.5	80246	US-09-078-294-4	Sequence 4, Appl
C 44	38.8	1.5	80595	US-09-078-294-3	Sequence 3, Appl
C 45	38.8	1.5	90050	US-09-245-041-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-222-177A-24/c
Sequence 24, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n. (dg-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865,601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Caucasian
TISSUE TYPE: Blood
IMMEDIATE SOURCE:
CLONE: Mtd40
POSITION IN GENOME:

```

ADDRESS: Foley & Lardner  

STREET: 1800 Diagonal Road, Suite 500  

CITY: Alexandria  

STATE: VA  

COUNTRY: USA  

ZIP: 22313-0299  

COMPUTER READABLE FORM:  

MEDIUM TYPE: Floppy disk  

OPERATING SYSTEM: IBM PC compatible  

SOFTWARE: Patentin Release #1.0, Version #1.25  

CURRENT APPLICATION DATA:  

APPLICATION NUMBER: US/08/232,463  

FILING DATE:  

CLASSIFICATION: 43S  

PRIORITY APPLICATION DATA:  

APPLICATION NUMBER: US/07/935,313  

FILING DATE:  

APPLICATION NUMBER: EP 91 114 300.6  

FILING DATE: 26-AUG-1991  

ATTORNEY/AGENT INFORMATION:  

NAME: BENT, Stephen A.  

REGISTRATION NUMBER: 29,768  

REFERENCE/DOCKET NUMBER: 30472/114 IMMU  

TELECOMMUNICATION INFORMATION:  

TELEPHONE: (703)836-9300  

TELEFAX: (703)683-4109  

TELEX: 899149  

INFORMATION FOR SEQ ID NO: 14:  

SEQUENCE CHARACTERISTICS:  

LENGTH: 7218 base pairs  

TYPE: nucleic acid  

STRANDEDNESS: single  

TOPOLOGY: linear  

IMMEDIATE SOURCE:  

CLONE: pTZgc-Fl6  

US-08-232-463-14

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Query Match 1.7%; Score 45.2; DB 1; Length 7218;
Best Local Similarity 5.2%; Pred.No. 0.01;
Matches 20; Conservative 202; Mismatches 160; Indels 0; Gaps 0;

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DB	1020 CACAAGATTAAATTCGAGCTTGCTGCAGGTGAGGAGCTTGCGATYYYYYYYYYY	1079
QY	390 AGGCTCCCTGGAGCATCTCTATCTCATTCAGCGCCATACTACCAGTC	449
DB	1080 YYYYYYYYYYYYYYYY	1139
QY	450 TAATATGAATGAGGACAGCCCTCTTTCTGTGAATTCACCTCGCAGGGTGACTCG	509
DB	1140 YYYYYYYYYYYY	1199
QY	510 TGAAGAACAGAAGTAAGCTCGGTGTATTTTCAGCACGCTAAGCACAGGCTCTCCGANT	569
DB	1200 YYYYYYYYYYYY	1259
QY	570 TTCAGCTCTTCCCATTAATTTCCCTCGGGCGAGAGGACTAGCATTTGCGCAC	629
DB	1260 YYYYYYYYYYYY	1319
QY	630 CCAGCTCTGCGCTGTTTTTATGACTTTGTCAAATTAAGCTTGTTCATTTCT	689
DB	1320 YYYYYYYYYYYY	1379
QY	690 GAATGTGTGATGCTGCTTC	711
DB	1380 YYYYYYYYYYYY	1401

RESTLT 11
US-08-222-177A-169/c
; Sequence 169, Application US/08222177A
; Patent No. 5,582,979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460

[illegible]

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ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3854 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-720-484A-1

Query Match          1.6%; Score 40.8; DB 2; Length 3854;
Best Local Similarity 81.9%; Pred. No. 0.14;
Matches 59; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Cy      998 TCTGTCGTCTCCATCATCTGAAGTACGTGCTGCTGCTGCT -TTTGCTGCTGCTGCTGCT 1056
Db      3522 TCTCTTGAGACCACCACTCGAAGTAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3463
        |||||
Qy      1057 GTGTGTGTGTGT 1068
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Db      3462 GTGTGTGTGTGT 3451

RESULT 13
US-08-953-823A-1/c
Sequence 1, Application US/08953823A
Patent No. 6136958
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothed Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,823A
FILING DATE: 30-Sep-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027070
FILING DATE: 30-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3854 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-953-823A-1

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GenCore version 5.1.4 ps 4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:36:08 ; Search time 523.407 Seconds
(without alignments)
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Title: US-09-778-971-4

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2589	100.0	2589	22	AAD13446
2	1472.2	56.9	1963	22	AAD13445
3	644.8	24.9	1701	21	AA87757
4	644.8	24.9	1701	22	AA64039
5	644.8	24.9	1796	24	AA518126
6	644.8	24.9	1818	22	AAD12581
7	644.8	24.9	2161	22	AAH99008
8	643.2	24.8	1713	24	ABH03202
9	643.2	24.8	1837	22	AAD13443

10	643.2	24.8	1841	24	AAD28776	Human interleukin-
11	643.2	24.8	1841	24	ABA03200	Human IL-17 recept
12	643.2	24.8	2015	24	AAD28777	Human interleukin-
13	643.2	24.8	2015	24	ABA03201	Human IL-17 recept
14	632.8	24.4	1918	21	AA575772	CDNA encoding a hu
15	632.8	24.4	1918	21	AA52046	CDNA encoding inte
16	632.2	24.4	637	24	AA518128	Mouse DNA cytokin
17	625.6	24.2	1515	22	AA546124	Human DNA encoding
18	625.6	24.2	1515	22	AA509514	Human CDNA encodin
19	625.6	24.2	1515	22	AA592136	Human PRO5801 CDNA
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21	625.6	24.2	1816	21	AA52035	CDNA encoding inte
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24	498.6	19.3	2725	24	ABL61567	Human interleukin
25	498.6	19.3	2856	22	AAD13444	Human interleukin-
26	434.6	16.8	2080	21	AA595789	Human immune syste
27	382	14.8	32177	22	ABA18493	Human immune syste
28	382	14.8	32177	22	AA529828	Human nervous syst
29	382	14.8	32177	22	AA529828	Human cytoskeletal
30	360.4	13.9	714	20	AA205374	Human reproductive
31	287.4	11.1	603	24	ABO59113	Human IL-17RH CDNA
32	218	8.4	471	24	ABO58257	Human colon cancer
33	149.2	5.8	210	24	AA518129	Human colon cancer
34	147.6	5.7	374	22	AA598686	Mouse DCR66 revers
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36	130.8	5.1	409	21	AA52036	CDNA clone sequenc
37	130.8	5.1	409	21	AA235747	HPC63R CDNA clon
38	113.6	4.4	327	21	AA575763	Human interleukin
39	113.6	4.4	327	21	AA52037	CDNA clone sequenc
40	113.6	4.4	327	21	AA535748	HERC45RA CDNA clo
41	65	2.5	65	24	ABN54635	Human interleukin
42	50.4	1.9	6012	24	ABL70463	Mouse spliced tran
43	50.4	1.9	6012	24	ABK1490	Chemically treated
44	50	1.9	5398	24	ABL32143	Signal transductio
45	46.6	1.8	259	18	AA565675	Human immune syste

ALIGNMENTS

RESULT 1	
AAD13446	
ID AAD13446	strand; CDNA; 2589 BP.
XX	
AC AAD13446;	
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DT 06-NOV-2001	(first entry)
DE	
XX	Mouse interleukin-17 receptor related protein (EV127) encoding CDNA #2.
XX	
KW	Mouse; interleukin-17 receptor related protein; IL-17; chromosome 14;
KW	EV127; retroviral integration; chromosomal mapping; mutational analysis;
KW	BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-6; therapy;
KW	haematopoietic cell; cancer; autoimmune disease; ss.
XX	
OS	Mus sp.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	19..1511
FT	/*tag= d
FT	/product= "Mouse EV127 protein"
FT	/transl_except= "(pos:162..163, aa:Cys-Leu)"
FT	/note= "Insertion of 626 bases alters the reading
FT	frame; CDS does not include stop codon"
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XX	
XX	MO200157202-A2.
XX	
XX	09-AUG-2001.
XX	
XX	PD
XX	
XX	02-FEB-2001; 2001WO-US03518.
XX	

PR	04-FEB-2000; 2000US-0180374.
XX	(UTAR-) UNIV ARKANSAS.
PA	
XX	Shaughnessy JD;
P1	
XX	WPI; 2001-496920/54.
DR	P-PsDB; AAE07163.
XX	New nucleic acids encoding an interleukin (IL)-17 receptor related
PT	protein for use as a marker for leukemia
XX	
PS	Claim 1a; Page 77-78; 87pp; English.
XX	
CC	The present sequence is a cDNA encoding mouse interleukin (IL)-17
CC	receptor related protein (Evi27). Mouse Evi27 gene was mapped to
CC	chromosome 14. Evi27 is a common site of retroviral integration
CC	in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful
CC	as antisense molecules to inhibit Evi27 protein or for chromosomal
CC	mapping or mutational analysis of Evi27 protein. They are proviral
CC	integration sites associated with leukaemias and monitoring this
CC	site provides a genetic tag for disease gene identification. The
CC	proteins of the invention are useful to stimulate the secretion of
CC	proinflammatory cytokines such as IL-8 and plays an important role
CC	in the development and/or disease processes of hematopoietic
CC	cells. Hence modulating the expression of Evi27 at the RNA or
CC	protein level is used in the treatment of diseases such as cancer
CC	or autoimmune diseases.
SQ	
	Sequence 2589 BP; 642 A; 628 C; 643 G; 676 T; 0 other;
	Query Match 100.0%; Score 2589; DB 22; Length 2589;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2589; Conservative 0; Mismatches 0; Indels 0; Gaps
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Db	121 ATGTGTCACAACAACAACACTCTCTCCAGAGACTTGAGGGAGCTTCCAAGTGAATCTGTCAG 180
OY	181 ACAAGTGTGGCAGCAGAGAGAATTTCAATTTGATGATAAATAGCTGATCTCCGGGCA 240
Db	181 ACAAGTGTGGCAGCAGAGAGAATTTCAATTTGATGATAAATAGCTGATCTCCGGGCA 240
OY	241 GACGCCAGCATCCGCTTGTGTAAGGCCACCAAGATCTGGGTGAGTGGCAAAAACAACATG 300
Db	241 GACGCCAGCATCCGCTTGTGTAAGGCCACCAAGATCTGGGTGAGTGGCAAAAACAACATG 300
OY	301 AATTCAATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACAGACT 360
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Db	361 TCCGGGGGCAATGAGCAATTTCTCATATGAGGCTTCCGTGGAGGTGAGCACTCTCAT 420
OY	421 CTCATCAGCGCCCATTAACAATCCCAATGCTAATATGATAGAGACAGGCCCTTCTTGTCT 480
Db	421 CTCATCAGCGCCCATTAACAATCCCAATGCTAATATGATAGAGACAGGCCCTTCTTGTCT 480
OY	481 GTGAACCTTCACTTCGCGAGGTGCACTGTGTAAAAACAAGAAATACGTCGGGTGATTT 540
Db	481 GTGAACCTTCACTTCGCGAGGTGCACTGTGTAAAAACAAGAAATACGTCGGGTGATTT 540
OY	541 CGAGAGCTTAACACCAAGGCTCTCGGATTTTCACTCTTTCCTTCAATTAATTTCTCTCT 600
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[illegible]

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QY 1681 GTGCTTCACTGACTTTCTTCAAAACTACTGCGAAGTGAAGTCTTGTGAATAATGCG 1740
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DB 1741 AGAAAAAGAAAAATGCGCGAGATGGGGCGGTACAGTGGCTGACCACTCAGAACCAAGCGG 1800
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DB 1801 CAGATAAAGTGTCTTCTTCTTCCAGTAGACGTCCGACCCCTTGTGACAGTGCCTGTG 1860
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QY 1981 GGGAGAGAGACTCAAAAGGCGACTATTAATGCTGAGTGTCTGCGCCCAATATCATCTCA 2040
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QY 2041 TGAAGAGCGCCAGAGCTTTTCCACAGAACTTCTCAAGGCTACGACAGCATGTCAAGTGA 2100
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QY 2581 AAAAAAAAAA 2589
DB 2581 AAAAAAAAAA 2589

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RESULT 2
AADI3445
ID AADI3445 standard; cDNA; 1963 BP.
XX
AC AADI3445;
XX
DT 06-NOV-2001 (first entry)

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XX DE Mouse interleukin-17 receptor related protein (Evi27) encoding cDNA #1.
XX
XX KW Mouse; interleukin-17 receptor related protein; IL-17; chromosome 14;
XX Evi27; retroviral integration; chromosomal mapping; mutational analysis;
XX KW BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-6; therapy;
XX KW haematopoietic cell; cancer; autoimmune disease; ss.
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XX OS Mus sp.
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XX CDS 19..1518
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XX PD 09-AUG-2001.
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XX PF 02-FEB-2001; 2001WO-US03518.
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XX PA (UNPAR-) UNIV ARKANSAS.
XX
XX PI Shaughnessy JD;
XX
XX DR WPI; 2001-496920/54.
XX
XX DR P-PSDB; AAE07162.
XX
XX PT New nucleic acids encoding an interleukin (IL)-17 receptor related
XX protein for use as a marker for leukemia
XX
XX PS Claim 1a; Page 76-77; 87bp; English.
XX
XX CC The present sequence is a cDNA encoding mouse interleukin (IL)-17
XX receptor related protein (Evi27). Mouse Evi27 gene was mapped to
XX chromosome 14. Evi27 is a common site of retroviral integration
XX in BXH2 murine myeloid leukaemia. Evi27 cDNA sequences are useful
XX as antisense molecules to inhibit Evi27 protein or for chromosomal
XX mapping or mutational analysis of Evi27 protein. They are proviral
XX integration sites associated with leukaemias and monitoring this
XX site provides a genetic tag for disease gene identification. The
XX CC proteins of the invention are useful to stimulate the secretion of
XX CC proinflammatory cytokines such as IL-6 and plays an important role
XX CC in the developmental and/or disease processes of haematopoietic
XX CC cells. Hence modulating the expression of Evi27 at the RNA or
XX CC protein level is used in the treatment of diseases such as cancer
XX CC or autoimmune diseases.
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XX Query Match 56.9%; Score 1472.2; DB 22; Length 1963;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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XX DB 487 TTCACCTGCGCAGGCTGCTTAACCAAGTAATATTAATAAGGACGTCAGGCG 546
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XX QY 1173 GGAAGCTGTGGAGCCAGACATCACTGTTGTAAGAAGAGAGTGGTGAAGTG 1232
XX DB 547 GGAAGCTGTGGAGCCAGACATCACTGTTGTAAGAAGAGAGTGGTGAAGTG 606
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XX DB 607 AATTTCAGAACCAATCCCTTGGAAACAGATTCAGATTCTAATGAGGACAGACA 666

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Oy	1353	ACTGAGAGAGTGAAGGTGCGGTGTTCAGCTGAACCCCATATTTACATACCTGCGCAAT	1412
Db	727	ACTGAGAGAGTGAAGGTGCGGTGTTCAGCTGAACCCCATATTTACATACCTGCGCAAT	786
Oy	1413	GACTGCATCCGACCGGAAGGGACAGTTGTCTTTCCTCAGAGACAGTGTCTCCATCCCT	1472
Db	787	GACTGCATCCGACCGGAAGGGACAGTTGTCTTTCCTCAGAGACAGTGTCTCCATCCCT	846
Oy	1473	CCAGATGACAAACAGACGATCTCTGGAGAGCTGAGCTGCTCTCTTCTGTGTCTGTGGTG	1532
Db	847	CCAGATGACAAACAGACGATCTCTGGAGAGCTGAGCTGCTCTCTTCTGTGTCTGTGGTG	906
Oy	1533	GCTGTGTGGGTGCTGGACGCTGGGATCTACCTAATTGAGGCAAGAGAGACGACGAG	1592
Db	907	GCTGTGTGGGTGCTGGACGCTGGGATCTACCTAATTGAGGCAAGAGAGACGACGAG	966
Oy	1593	ACGTCCTTTTCCATTTTCCACATGCTCTCTGCCCCCTCATTTAAGGTCTGTGGTTATCCT	1652
Db	967	ACGTCCTTTTCCATTTTCCACATGCTCTCTGCCCCCTCATTTAAGGTCTGTGGTTATCCT	1026
Oy	1653	TCTGAGATATGTTTCCATCAACGCGTGTGTGCTTCACTGACCTTCTTCAAACTACGTC	1712
Db	1027	TCTGAGATATGTTTCCATCAACGCGTGTGTGCTTCACTGACCTTCTTCAAACTACGTC	1086
Oy	1713	AGAACTGAGGTCTATCTTTGAAAAATGGCAGAAAAAATCGCCAGATGGGGCCGGTA	1772
Db	1087	AGAACTGAGGTCTATCTTTGAAAAATGGCAGAAAAAATCGCCAGATGGGGCCGGTA	1146
Oy	1773	CAGTGGCTGACCACTCAGAGCAAGCGGCAAGATPAAAGTGTCTTCTTCCAGTGAC	1832
Db	1147	CAGTGGCTGACCACTCAGAGCAAGCGGCAAGATPAAAGTGTCTTCTTCCAGTGAC	1206
Oy	1833	GTCCCGACCCCTTGTGACAGTGCCTGTGGGCAAAAGAGGGGACGCGACGGAGAACTCT	1892
Db	1207	GTCCCGACCCCTTGTGACAGTGCCTGTGGGCAAAAGAGGGGACGCGACGGAGAACTCT	1266
Oy	1893	CAGATCTGTTCCCTCTGTGCTTAAACCTTTTGTAGTATTTACAGCAGCCAGACGAT	1952
Db	1267	CAGATCTGTTCCCTCTGTGCTTAAACCTTTTGTAGTATTTACAGCAGCCAGACGAT	1326
Oy	1953	CTGCACAAATACCTGTGTCTATCTTTGGGGAGCAGACCTPAAAGCGACTATATATCC	2012
Db	1327	CTGCACAAATACCTGTGTGTCTATCTTTGGGGAGCAGACCTPAAAGCGACTATATATCC	1386
Oy	2013	CTGAGTGTCTGCCCCCAATATCATCTCATAGAGAGCCACAGCTTTTCAACAGAACTT	2072
Db	1387	CTGAGTGTCTGCCCCCAATATCATCTCATAGAGAGCCACAGCTTTTCAACAGAACTT	1446
Oy	2073	CTCAAGGCTACGACAGACAGTGTCAGTGAAAGAAACGCTCAAGGCTGCGCATATAGCTGT	2132
Db	1447	CTCAAGGCTACGACAGACAGTGTCAGTGAAAGAAACGCTCAAGGCTGCGCATATAGCTGT	1506
Oy	2133	TCACCTGTATGTCCACC CGGGGAATAGAGCTCTGAAGCCTTCTCTACTCTCCCTTCCA	2192
Db	1507	TCACCTGTATGTCCACC CGGGGAATAGAGCTCTGAAGCCTTCTCTACTCTCCCTTCCA	1566
Oy	2193	GTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGAGAGGCTGTGTGAGGTATGTCT	2252
Db	1567	GTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGAGAGGCTGTGTGAGGTATGTCT	1626
Oy	2253	ATGTACAAACTGTGTTTAAAACTGGAGTTTGGCAAACTCAACTGAGCATPACACGCTGAG	2312
Db	1627	ATGTACAAACTGTGTTTAAAACTGGAGTTTGGCAAACTCAACTGAGCATPACACGCTGAG	1686
Oy	2313	GCTAGCTATTTGGCTGATTTATGAGACAAACAGTTACAGACAAATPAAATGAGTGGAGCT	2372
Db	1687	GCTAGCTATTTGGCTGATTTATGAGACAAACAGTTACAGACAAATPAAATGAGTGGAGCT	1746
Oy	2373	ACATTTGGGATATACCCAAAGCTGGGTATGATTTATCACTGAGAACACGCACTTGTGCC	2432

Dd	1747	ACATTGGGATATACCAGAACTGGGTATATATTATCACTGAGAACACGACTCTGCC	1806
Oy	2433	ATGAAGTAATACGCAGCTTCCCTGTCAAGCTGTCTGCAGTTGGGTCTGTCCTGACTG	2492
Dd	1807	ATGAAGTAATAACGCGACTTCCCCTGTCAAGCTGTCTGCAGTTGGGTCTGTCCTGACTG	1866
Oy	2493	CCCATGCTCTAATNGCTGCGACGTAGACCCGTTTGTAACAATTTAATCTGTTATGAATATC	2552
Dd	1867	CCCATGCTCTAATNGCTGCGACGTAGACCCGTTTGTAACAATTTAATCTGTTATGAATATC	1926
Oy	2553	CGTTTGGAGAGCTCTCAAAAAAAAAAAAAAAA 2589	
Dd	1927	CGTTTGGAGAGCTCTCAAAAAAAAAAAAAAAA 1963	
 RESULT 3 AAAA87757			
XX	ID	AAA87757 standard; cDNA; 1701 BP.	
XX	AC	AAA87757;	
XX	DT	28-NOV-2000 (first entry)	
XX	DE	Human secreted protein encoding cDNA SEQ ID #56.	
XX	KW	Human; secreted protein; forensic procedure; gene therapy;	
XX	KM	chromosome mapping; cancer; autoimmune disease; cardiovascular disorder	
XX	KW	cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;	
XX	KM	brain disorder; skeletal muscle disorder; eye disorder; obesity;	
XX	KW	mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease;	
XX	KM	neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;	
XX	KW	septic shock; impotence; ss.	
XX	OS	Homo sapiens.	
XX	FN	WO200037491-A2.	
PD	PN	29-JUN-2000.	
XX	PF	20-DEC-1999; 99WO-IB02058.	
PR	PR	22-DEC-1998; 98US-0113686.	
PA	PA	25-JUN-1999; 99US-0141032.	
XX	(GENST) GENSET.		
PI	Bougueleret L, Dumas J, Duclert A;		
DR	WIPI; 2000-442637/38.		
DR	P-PSDB; AAB25795.		
PT	Polynucleotides and polypeptides encoding proteins with signal		
PT	peptides, useful in diagnostic, forensic, gene therapy and chromosome		
PT	mapping procedures -		
PS	Claim 1; Page 221-223; 306pp; English.		
CC	This sequence represents human cDNA encoding a secreted protein. The		
CC	invention relates to sequences AAA87725-A87774 which encode human		
CC	secreted proteins AAB25763-B25812. The proteins include signal peptides		
CC	included in the invention are a host cell containing one of the cDNA		
CC	sequences, and a purified antibody capable of binding to one of the		
CC	secreted proteins. Also contained in the invention are methods for		
CC	storing the sequence data on a computer system, and a method for		
CC	identifying features of the cDNA sequences using a computer programme.		
CC	The cDNAs are useful for expressing secreted proteins or fragments to		
CC	obtain antibodies capable of specifically binding to the secreted		
CC	proteins. The cDNAs may also be useful in diagnostic, forensic, gene		
CC	therapy and chromosome mapping procedures and may be used to design		
CC	expression vectors and secretion vectors. The proteins of the invention		
CC	may be used to treat diseases including cancer, autoimmune diseases,		
CC	cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological		


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QY 1293 TTGGGGTTTCTAGAGTCTGG-----AGATAAACTGATGAGCAGCTGTGAGCC 1343
DB 542 ATCCGGTTTCTCAGGTGTGTTGAGCCACACAGAAAGAAACAAAGCGAGCTTCAAGTGTG 601
QY 1344 ATCCGGGTGATGAGAGAGTGAAGGTGGGTGTTCAAGTGTGAGCCCTATTATTAATACC 1403
DB 602 ATTCAGTGTGAGTGAAGTGAAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 661
QY 1404 TGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
DB 662 TGTCGCAAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 721
QY 1464 CCATGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1523
DB 722 CTTTCCCTCTGATTAACAACAAAGCAAGCGGAGGCTGGCTGCTCTCTCTCTCTCTCTCT 781
QY 1524 ---GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1580
DB 782 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
QY 1581 AGGAGCAGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1640
DB 842 AGGATCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 898
QY 1641 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1700
DB 899 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 958
QY 1701 CAAATCTACTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1760
DB 959 CAAATCTACTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1018
QY 1761 ATGGGGCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1820
DB 1019 ATGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1078
QY 1821 CTTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1880
DB 1079 CTTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1138
QY 1881 AGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1940
DB 1139 AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1198
QY 1941 AGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2000
DB 1199 AGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1258
QY 2001 GACTAATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2060
DB 1259 GACTAATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1318
QY 2061 CACGCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2120
DB 1319 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1378
QY 2121 CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2178
DB 1379 CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1438
QY 2179 TACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
DB 1439 TATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1480

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RESULT 5
AAS18126
ID AAS18126 standard; cDNA; 1796 BP.
XX
AC AAS18126;
XX
DT 26-MAR-2002 (first entry)
XX

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DE Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA.
XX
KM Human: DNAX cytokine receptor subunit 6; DCRS6; phosphate labelling; ss;
KM gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4..1512
FT /tag= a
FT /product= "Human DCRS6"
XX
PN WO200190358-A2.
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16767.
XX
PR 24-MAY-2000; 2000US-206862P.
XX
PA (SCHE ) SCHERING CORP.
PI Gorman DM;
XX
DR MPI; 2002-106198/14.
DR P-PSDB; AUI1351.
XX
PT Isolated antigenic human or mouse DNAX receptor subunit-like
PT polypeptide useful for detecting antibodies generated in response to
PT presence of increased protein levels or immunological disorders -
XX
PS Disclosure; Page 7-10; 148bp; English.
XX
CC The invention relates to primate and rodent DNAX cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes
CC to label general or specific substrates. The subunits may also be
CC functional immunogens to elicit recognising antibodies, or antigens
CC capable of binding antibodies. A combination, e.g., including a DCRS can
CC be used as an immunogen for the production of antisera or antibodies
CC capable of distinguishing between other cytokine receptor family members.
CC A purified DCRS can also be used as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to antibody production to the
CC endogenous receptor. This sequence represents cDNA encoding the human
CC DCRS6 polypeptide.
XX
SQ Sequence 1796 BP; 514 A; 439 C; 399 G; 444 T; 0 other;
XX
Query Match 24.9%; Score 644.8; DB 24; Length 1796;
Best Local Similarity 76.0%; Pred. No. 5..5e-182;
Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;

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QY 1113 TTTCACATTCCTCCAGCTGCTTAAACACGTAATGTAATATTAATAAAGAGTGTGAGCGC 1172
DB 472 TTTCACATTCCTCCAGCTGCTTAAACACGTAATGTAATATTAATAAAGAGTGTGAGCGC 531
QY 1173 GGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232
DB 532 GGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
QY 1233 AATTTCACAAACCAATCCCTTGAAGACATGATGATGATGATGATGATGATGATGATGAT 1292
DB 592 AATTTCACAAACCAATCCCTTGAAGACATGATGATGATGATGATGATGATGATGATGAT 651
QY 1293 TTGGGGTTTCTAGAGTCTGG-----AGATAAACTGATGAGCAGCTGTGAGCC 1343
DB 652 ATCCGGTTTCTCAGGTGTGTTGAGCCACACAGAAAGAAACAAAGCGAGCTTCAAGTGTG 711
QY 1344 ATCCGGGTGATGAGAGTGAAGGTGGGTGTTCAAGTGTGAGCCCTATTATTAATACC 1403
DB 712 ATTCAGTGTGAGTGAAGTGAAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 771

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QY 1173 GGAAGCTGTGGAGCCAGACATCACTGCTGTATAAAGAAAGAGAGATGGTGAAGTG 1232
DB 554 GGAAGCTGTGGAGATCCGAACATCACTGCTGTATAAAGAAAGAGAGATGGTGAAGTG 613
QY 1233 AATTTCACAAACCAATCCCTTGGAAACAGATACAGATTCATTCATTCACAGGACACACA 1292
DB 614 AACTTCACAAACCACTCCCTGGGAAACAGATACATGGCTCTTATTCACACAGCATATC 673
QY 1293 TTGGGGTTTTCTAGAGTCTGG-----AGATAAACTGATGAGAGACGTGTAGACC 1343
DB 674 ATCGGGTTTTCTCAGAGTGTGGAGCACACAGAGAAAGAAACAAAGCAGCTTCAGTGTG 733
QY 1344 ATCCCGGTGACTGAGAGAGTGAAGGTGGCGGTGTGCTGAGCTGACGCCATATTTACATACC 1403
DB 734 ATTCAGAGTGACTGGGAGATGAGAGGTGTACGGTGCAGCTGATCCATATTTTCTACT 793
QY 1404 TGGGGCAATGATCTGATCCACCGGAGAGGACATTTGTGCTTGTCTAGAGACAAAGTCT 1463
DB 794 TGTGGCAGCAGTGCATCCGACATPAAAGAAACAGTTGTGCTGTGCGCAAAACAGCGCTC 853
QY 1464 CCCATCCCTCCAGATGACAAACAGACGATGCTGGAGGCTGTGCTCTTCTCTGTG 1523
DB 854 CTTTCCCTCTGATTAACAACAAAGCAGCGGAGGCTGTGCTCTCTCTCTGTG 913
QY 1524 ---CTGCTGTGCTGTGTGGGTGCTGGCAGCTGGATCTAACCTGAGGAGGACGAA 1580
DB 914 TCTGTGCTGTGGCCACATGGGTCTGTGGCAGGAGATCTATATGTGAGGACGAA 973
QY 1581 AGAGAGCAGAAAGCTCTTCTTCCATTTCCACCAATGCTCCGCCCCCATTAAGTCTTG 1640
DB 974 AGGATCAAGAAAGACTCTCTTTCTA---CCACCACTACTGCCCCCATTAAGGTCCT 1030
QY 1641 GTGGTTATCTCTGATATATGTTTCCATACACACCGTGTGCGCTTCACTGACTTCTT 1700
DB 1031 GTGGTTATACCATTGAAATATGTTTCCATACACATTTGTTACTTCACTGATTTCTT 1090
QY 1701 CAAAACCTACTGACAGAGTGAAGTCACTCTTGAATAATGGCAAAAAGAAATGCGCGAG 1760
DB 1091 CAAAACCATTTGACAGAAAGTGAAGTCACTCTTGAATAATGGCGAGAAATAGCAGAG 1150
QY 1761 ATGGGGCCGTTACGATGCTGACACATCTCAGAGCAAGCGGCAATTAAGTGTCTTCTT 1820
DB 1151 ATGGGTCTCAGTGAAGTGTGCTTGCACCTCAAAAGAGCAGACGAAAGTCTTCTTCTT 1210
QY 1821 CTTCCCAAGTACGTCGACCCCTTGTGACAGTGTCTGTGGCCCAATGAGGAGCGCC 1880
DB 1211 CTTTCCATATACGTCAACAGATGTGTGAGATGTAACCTGTGGCAAGAGCGAGGCTCC 1270
QY 1881 AGGAGAACTCTCAGAGATGTTGCTCTTCTTGAACCTCTTTTGTAGTGAATTCAGC 1940
DB 1271 AGTGAAGAACTCTCAAGACCTCTTCCCTTGTAACTTTTCTGCAGTGATCTAAGA 1330
QY 1941 AGCCAGACGATCTGCAACAAATCCTGTGTCTATCTTGGGGAGAGACCTCAAGGC 2000
DB 1331 AGCCAGATTTATCTGCAAAATACGTGTGTCTACTTTAAGAGATTGATCAAAAGAC 1390
QY 2001 GACTATATCCCTGAGTGTCTGCCCCCAATATCATCTCAATGAAGACGCGACAGCTTTC 2060
DB 1391 GATTACATGCTCTCAGTGTCTGCCCCAAGTACCACTCATGAAAGATGCACTGCTTTC 1450
QY 2061 CACACAGAACTTCTCAAGGCTTAGCGAGAGATGTCAGTGAAGAAAGCGCTCAAGCTGC 2120
DB 1451 TGTGCAAGAACTTCTCCATGTCTCAAGCAGAGATGTCAGCAAGAAAGATCAAGCTGC 1510
QY 2121 CAGATATGCTTCAACCTTGTAGTCAACCGGGGGA--TAAGATCTGAAGCTTTC 2178
DB 1511 CAGATATGCTGTCTCTGTTGTAGCCCAACCATGAGAAAGAGAGACTTAAAGGCTTTC 1570
QY 2179 TACTCTCCCTTCAGTGAACAATGCTGTGAGACACTTGAA 2220
DB 1571 TATCCACCAATTAAGGGAAGAAAGCTGTGATGATCTTGA 1612

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RESULT 7
ID AAH99008
ID AAH99008 standard; cDNA; 2161 BP.
XX
AC AAH99008;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 865.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN MO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001MCO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617446.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSF-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
XX
P-PSDB; AAM24349.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 707; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 2161 BP; 639 A; 516 C; 446 G; 560 T; 0 other;
XX
Query Match 24.9%; Score 644.8; DB 22; Length 2161;
Best Local Similarity 76.0%; Pred. No. 6; 1e-182; Indels 17; Gaps 4;
Matches 853; Conservative 0; Mismatches 252;
XX
QY 1113 TTCACATTCCTCCAGGCTGCTTAACCAAGTAATGAATTAAGACAGTGCATGAGCG 1172
DB 476 TTCACCTACACAGGCTGCTTAACCAAGTAATGAATTAAGACAGTGCATGAGCGC 535
QY 1173 GGAAGCTGTGGAGCCAGACATCACTGCTGTATAAAGAAAGAGAGATGGTGAAGTG 1232
DB 536 GGAAGCTGTGGAGATCCGAACATCACTGCTGTATAAAGAAAGAGAGATGGTGAAGTG 595
QY 1233 AATTTCACAAACCAATCCCTTGGAAACAGATACAGATTCATTCACAGGACACAGACA 1292
DB 596 AACTTCACAAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGCACTATC 655
QY 1293 TTGGGGTTTTCTAGAGTCTGG-----AGATAAACTGATGAGAGCGTCTGAGCC 1343
DB 656 ATCGGGTTTTCTCAGTGTGTTGAGCCACACGAAAGAAACAAAGCGAGCTTCAAGTGTG 715
QY 1344 ATCCCGGTGACTGAGAGAGTGAAGGTGGGTGTTCAAGCTGACCCCATATTTACATACC 1403

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Db 716 ATTCAGAGCTGGGATATGAAAGGTGACGCTGACGTGATCTCATATTTTCTACT 775
1404 TGGGGAATAGCTGATCCGACCGGAAGGACAGTTGTGCTTTGCTCAGAGCAAGTGT 1463
776 TGTGGCAGCAGCTGATCCGACATMAAGGAACAGTTGTGCTGTGCCCAAAAGGCTC 835
1464 CCCATCCCTCAGATGCAACAGACGATGCTGGAGAGCTGCTGCTCTCTTCTGTG 1523
836 CTTTCCCTCTGATTAACAACAAAGCAAGCCGGAGAGCTGGCTGCTCTCTCTGCTG 895
1524 ---CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1580
896 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
1581 AGGAGACGGAAGAGTCTCTTCTTCTATTTCCACATGCTCTGCCCCCTATTAAAGTCTG 1640
956 AGGATCAAGAGAGCTTCTTCTTCTA---CCACCACTACTGCCCCCATTAAGTCTT 1012
1641 GTGGTTATCTCTGATATGTTTCCATCAGACCGTGTGCTGCTCACTGACTTCTT 1700
1013 GTGGTTATCCCATCTGAATATGTTTCCATCAGACATTTGTTACTTCACTGAATTTCT 1072
1701 CAAACTACTGCAAGAGTGTGATCTTGAATAATGCGAAGAAAGAAATGCGCGAG 1760
1073 CAAACCATTTGCAAGAGTGTGATCTTGAATAATGCGAAGAAAGAAATGCGAG 1132
1761 ATGGGGCGGTACAGTGTGACGACCTCAGACCAAGCGGCAATTAAGTGTCTTCTT 1820
1133 ATGGGTCAGTGTGATGTGCTTGCCTCAAAAGAGGACAGCAAAAGTGTCTTCTT 1192
1821 CTTCAGTGTGATGTGATGTGCTTGTGACAGTGTGCTGTGCGCAATGAGGCGAGCGC 1880
1193 CTTCAGTGTGATGTGATGTGCTTGTGACAGTGTGCTGTGCGCAATGAGGCGAGCGC 1252
1881 AGGAGAACTCTAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1940
1253 AGGAGAACTCTAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1312
1941 AGGAGAACTCTAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2000
1313 AGGAGAACTCTAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1372
2001 GACTATATGCTCTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2060
1373 GATTACAACTCTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1432
2061 CACACAACTCTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2120
1433 TGTGAGAACTCTGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1492
2121 CATGATAGCTGTGATCCCTGTGTGTGATCCACCGGGGGA--TAAGACTGTGAAGCTTCT 2178
1493 CAGATAGCTGTGATCCCTGTGTGTGATCCACCGGGGGAAGAGAGCTTAAAGGCTTCT 1552
2179 TACTCTCTCTCTGAGTGTGATCCCTGTGTGTGATCCCTGTGA 2220
1553 TATCCACCAATTAACAGGAAAAAAGTGTGATGATCTTGA 1594

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KW Interleukin 17; immune system disorder; infection; weight; reproductive;
KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
KW tumour; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 273..1430
FT /tag=a
FT /product="Human IL-17 receptor-like protein #3"
PN WO200168705-A2.
PD 20-SEP-2001.
PP 16-MAR-2001; 2001WO-US08688.
PR 16-MAR-2000; 2000US-189923P.
PR 12-MAY-2000; 2000US-204208P.
PR 27-NOV-2000; 2000US-0723232.
PR 02-FEB-2001; 2001US-266159P.
XX (AMGE-) AMGEN INC.
PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ,
DR MPI: 2002-055100/07.
DR P-PSDB; AAM47459.
XX
PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
PT polypeptides, useful for treating, diagnosing, ameliorating or
PT preventing immune system disorders (e.g. psoriatic arthritis) and
PT infections (e.g. viral infections) -
XX
PS Claim 1; Fig 5; 239p; English.
XX
CC The present invention relates to novel human nucleic acids encoding
CC interleukin 17 (IL-17) receptor like proteins. The present sequence is
CC one such coding sequence. The IL-17 receptor-like proteins and coding
CC sequences are useful for treating a pathological condition related to
CC immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction
CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.
CC ischaemia), eye disorders, reproductive disorders, tumours and
CC inflammation.
CC
SQ Sequence 1713 BP; 488 A; 419 C; 385 G; 421 T; 0 other;

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Query Match 24.8%; Score 643.2; DB 24; Length 1713;
Best Local Similarity 75.9%; Pred. No. 1.6e-181;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

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QY 1113 TTCACATTCCTCCAGGCTGCTTAACCAACGATATGAAATATATAAAGCAGTGCATGAGCG 1172
DB 390 TTCACCTCACAGGCTGCTTAACCAACGATATGAAATATATAAAGCAGTGCATGAGCG 449
QY 1173 GGAAGCTGTGGAGCCGACACATCACTGCTTGTAAAGAAAGAGAGTGTGAAGTG 1232
DB 450 GGAAGCTGTGGAGATCCGAACATCACTGCTTGTAAAGAAAGAGAGTGTGAAGTG 509
QY 1233 AATTTCACAACCAATCCCTTGTGAACATATCAGATTCTCATTTAAAGGAGACAGACA 1292
DB 510 AACTTCACAACCACTCCCTGTGGAAACAGATCATGTGCTTTATCCAAACAGCACTATTC 569
QY 1293 TTGGGGTTTCTAGAGTGTG-----AGAAATACTGATGAGAGCTGTGAGCC 1343
DB 570 ATCGGTTTCTCAGTGTGTTGAGCCACACAGAAAGAAACAGGAGCTTCAAGTGTG 629
QY 1344 ATCCCGTACTGAGAGAGTGAAGGTGGGTGTTCACTGACCTGACCCCATATTTTACATACC 1403

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RESULT 8
 ABA03202
 ID ABA03202 standard; cDNA; 1713 BP.
 AC ABA03202;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Human IL-17 receptor like protein #3 coding sequence.
 XX
 KW Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
 KW antiproliferative; antimicrobial; anorectic; neuroprotective;
 KW antiallergic; dermatological; cytostatic; gene therapy;

Db 630 ATTCAGTACTGGGGATAGTGAAGTGTCTACGGTGCAGCTGACTCCATATTTCTTACT 689
 Qy 1404 TGGCGCAATGATCTGCATCCGACGCGAAGGACAGTTGTCTTTGCTCAGAGCAAGTGTCT 1463
 Db 690 TGTGGCAGCGATCTGATCCGACATTAAGGAACAGTTGTCTCTGCTCCCAACAAAGGCTC 749
 Qy 1464 CCATTCCTCCAGATGACACAGACGATGTGGAGGCTGGCTGCTCTCTTCTCTGGTG 1533
 Db 750 CTTTCCCTCTGATTAACACAAAGCAAGCGGAGGCTGGCTGCTCTCTCTCTGCTG 809
 Qy 1524 ---CTGCGTGGTGTGTGTGGTGTGGCACTGGGATCTTACCTTAATCTTGGAGCAAGGA 1580
 Db 810 TCTCTGCTGGTGGCAACATGGGTGTGGTGGAGGATCTATCTTAATGTGAGCAAGAA 869
 Qy 1581 AGGAGCAGAGAGAGCTCTTCTTATTTCCACCATGTCTGCTGCTCCATTAAGTCTG 1640
 Db 870 AGATACAGAGAGACTCTCTTTTCTA---CAACCACTACTAGCTCCCATTAAGTCTT 926
 Qy 1641 GTGGTTATCTCTTGAGATATGTTTCCATACACCGTGTGTGCTTCACTGACTTTCTT 1700
 Db 927 GTGGTTATCCCATCTGAATATGTTTCCATCACCAATTTGTTCACTGAATTTCTT 986
 Qy 1701 CAAATCTACGACAGAGAGAGTCACTCTTGAATAAATGGGCAAGAAATGGCCGAG 1760
 Db 987 CAAATCTACGACAGAGAGTCACTCTTGAATAAATGGGCAAGAAATGGCAGAG 1046
 Qy 1761 ATGGGGCCGAGTACAGTGGCTGACCACTGAGAGCAAGCGGAGATTAAGTGTCTTCTT 1820
 Db 1047 ATGGGTTCAGTGCAGTGGCTTGGCTGCACTCAAAAGAGCAGAGCAAAAGTGTCTTCTT 1106
 Qy 1821 CTTTCCAGTGCAGTGGCCGACCTTTGTGACAGTGCCTGTGGCCAATGAGGCGAGGCC 1880
 Db 1107 CTTTCCAGTGCAGTGCAGTGTGTGGATGTACTGTGGCAAGCGAGGCGAGTCCC 1166
 Qy 1881 AGGAGAGTCTCAGATCTGTCTCTTCTTGAACCTTTGATGATTTGACG 1940
 Db 1167 AGTAGAGTCTCAGACCTCTTCTTCTTGAACCTTTGATGATTTGACG 1226
 Qy 1941 AGCAGAGCATCTGACAAATACCTGTGTCTATCTTGGGGGAGAGCACTCAAGAGC 2000
 Db 1227 AGCAGATTCATCTGCAAAATAGTGTGTCTACTTTAGAGATTTGATCAAAAGAC 1286
 Qy 2001 GACTATATGCTCTGAGTGTCTGCCCCCAATATCATCTCATGAGAGCCACGCTTTT 2060
 Db 1287 GATTACATGCTCTCAGTGTCTGCCCCCAATGACCACTCATGAGAGTGCACGCTTTT 1346
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 Db 1347 TGTGCAAGATCTTCTCAGTCAATGTCAGAGCAGAGTGTACAGAGAAAGATCAAGCCTGC 1406
 Qy 2121 CATGATAGTGTCTGACCTTGTATGTCACCCGGGGGAA--TAGAGCTCTGAAGCTTTC 2178
 Db 1407 CAGATGTGCTGTCTCTCTTGTAGCCCAATGAGAGCAAGAGACCTTAAAGGCTTTC 1466
 Qy 2179 TACTCTCCCTTCAAGTACAAATGCTGTGACGACTCTGA 2220
 Db 1467 TATCCCACTTACAGGAGAAACAGTGTATGATCTCTGA 1508
 RESULT 9
 AAD13443 ID AAD13443 standard; cDNA; 1827 BP.
 XX AAD13443;
 AC AAD13443;
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 DT 06-NOV-2001 (first entry)
 XX
 DE Human interleukin-17 receptor related protein (Evi27) encoding cDNA #1.
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 KW Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21;
 KW Evi27; retroviral integration; chromosomal mapping; mutational analysis;
 KW BXH2 murine myeloid leukemia; proinflammatory cytokine; IL-8; therapy;
 KW haematopoietic cell; cancer; autoimmune disease; ss.

XX Homo sapiens.
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 FH CDS 6..1514
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 FT sig_peptide /tag= a
 FT /product= "Human Evi27 protein"
 FT mat_peptide /tag= b
 FT 45..1511
 FT /tag= c
 FT /product= "Human mature Evi27 protein"
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 XX MO200157202-A2.
 PN
 XX
 PD 09-AUG-2001.
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 PF 02-FEB-2001; 2001WO-US03518.
 XX
 PR 04-FEB-2000; 2000US-0180374.
 XX
 PA (UYAR-) UNIV ARKANSAS.
 PI
 XX Shaughnessy JD;
 XX
 XX WPI; 2001-496920/54.
 DR P-PSDB; AAE07160.
 XX
 PT New nucleic acids encoding an interleukin (IL)-17 receptor related
 PS protein for use as a marker for leukemia
 PS
 PS Claim 1a; Page 74-75; 87bp; English.
 XX
 CC The present sequence is a cDNA encoding human interleukin (IL)-17
 CC receptor related protein (Evi27). Human Evi27 gene was mapped to
 CC chromosome 3p21. Evi27 is a common site of retroviral integration
 CC in BXH2 murine myeloid leukemias. Evi27 cDNA sequences are useful
 CC as antisense molecules to inhibit Evi27 protein or for chromosomal
 CC mapping or mutational analysis of Evi27 protein. They are proviral
 CC integration sites associated with leukemias and monitoring this
 CC site provides a genetic tag for disease gene identification. The
 CC proteins of the invention are useful to stimulate the secretion of
 CC proinflammatory cytokines such as IL-8 and plays an important role
 CC in the developmental and/or disease processes of haematopoietic
 CC cells. Hence modulating the expression of Evi27 at the RNA or
 CC protein level is used in the treatment of diseases such as cancer
 CC or autoimmune diseases.
 CC
 CC Sequence 1827 BP; 547 A; 438 C; 397 G; 445 T; 0 other;
 XX
 SQ
 Query Match 24.8%; Score 643.2; DB 22; Length 1827;
 Best Local Similarity 75.9%; Pred. No. 1.7e-181;
 Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;
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 Db 474 TTCACTTCCAGGCTGCTTAAACGATGAAATATTAAGAGCTGAGGGC 533
 Qy 1173 GGAAGCTGTGGAGCCCAACATCACTGCTTTGTAAGAAAGAGAGTGTGAAGT 1232
 Db 534 GGAAGCTGTGGAGTCCGAACATCACTGCTTTGTAAGAAAGAGAGTGTGAAGT 593
 Qy 1233 AATTGACAACCAATCCCTTGAAGACAGATTCATTTCAACGGGACAGACA 1292
 Db 594 AACTTCAACCACTCCCTTGGAAACAGATTCATTTCAACGGGACAGACA 653
 Qy 1293 TTGGGGTTTCTAGAGTGTG-----AGAAATAACTGATGAGAGCGTGTAGCC 1343
 Db 654 ATCGGGTTTCTCAGGTGTTTGAAGCAGACAGAGAAACAAAGCGAGCTTCAAGTGTG 713
 Qy 1344 ATCCCGGTACGAGAGAGTGAAGTGTGGGTGCTTCACTGACCTTATTTATACATACC 1403
 Db 714 ATTCAGTACGTGGGATAGTGAAGTGTCTAGGTGACGCTGACTTCATATTTTCTACT 773

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QY 1404 TCGCGCAATGACTGTCATCCGAGCGGAGACAGTTGTGCTTTGCTTCAGAGACAAGTGTCT 1463
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DB 834 CCTTCTCTCTGTGATTAACAACAAAGAGAGCGGAGGCTGTGCTCTCTCTCTCTGTG 893
QY 1524 ---CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1580
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DB 954 AGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
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QY 1701 CAAATCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1760
DB 1071 CAAATCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
QY 1761 ATGGGAGCGGATACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1820
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QY 1881 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940
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DB 1491 CATGATAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1550
QY 2178 TACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
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RESULT 10

AAD28776 standard; DNA; 1841 BP.

AAD28776;

07-MAY-2002 (first entry)

Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.

Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;
cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
inflammatory bowel disease; neuronal dysfunction; transplant rejection;
autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;

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KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
KW cancer; diabetes; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 50..1558  
FT /tag= a  
FT /product= "Human IL-17RB-2 protein"  
FT sig_peptide 50..92  
FT /tag= b  
FT mat_peptide 93..1555  
FT /tag= c  
FT /product= "Mature IL-17RB-2 protein"  
PN WO200208285-A2.  
PN 31-JAN-2002.  
PD 21-JUN-2001; 2001MO-US19861.  
PE 22-JUN-2000; 2000US-213125P.  
PR 02-FEB-2001; 2001US-266159P.  
PR 16-MAR-2001; 2001US-0810384.  
PA (AMGE-) AMGEN INC.  
PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S,  
PI WPI: 2002-155217/20.  
DR P-PSDB; AAE18127.  
XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
XX polypeptides useful in the treatment, prevention and diagnosis of  
XX diseases e.g. cancer  
XX  
XX Disclosure; Page 230-232; 242pp; English.  
XX  
XX The invention relates to nucleic acid molecules encoding Interleukin 17  
XX (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
XX of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
XX preventing or ameliorating a disease, such as immune system dysfunction  
XX (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
XX autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
XX disease, transplant rejection, graft vs. host disease); infections (HIV,  
XX hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
XX sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
XX (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
XX (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
XX (osteoporosis); Paget's disease; hypercalcaemia) vascular system (epilepsy  
XX atherosclerosis, heart failure, angiogenesis); tumour, cancers (lymphoma  
XX leukaemia); reproductive (infertility, miscarriage, endometriosis); eye  
XX (blindness, retinal neuropathy) and treatment of diseases involving  
XX inflammation. The present sequence is human Interleukin-17 receptor B-2  
XX (IL-17RB-2) DNA.  
XX  
SQ Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;

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Query Match 24.8%; Score 643.2; DB 24; Length 1841;

Best Local Similarity 75.9%; Pred. No. 1.7e-181;

Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

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QY 1113 TTCACATTCGAGGCTGCTTAACCAAGTAATGAATATTAAGAGAGAGAGAGAGAGAGAG 1172
DB 518 TTCACCTCACAGGCTGCTTAACCAAGTAATGAATATTAAGAGAGAGAGAGAGAGAGAG 577
QY 1173 GGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232
DB 578 GGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 637

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QY 1233 AATTTCACACCAATCCCTTGGAAAAGATACAGATTCCTATTCAACGGGACACGACA 1292
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QY 1464 CCCATCCCTCCAGATGACCAACAGACGATGCTGGAGGCTGGCTGCTCTTCTCTG 1523
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Db 878 CTTTCCCTCTGGATTAACAAACAAAGCAGCGAGGCTGGCTGCTCTCTCTCTG 937
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QY 1524 ---CTGCTGTGCTGTGTGGGTCTGGCAGCTGGGATCTTACTTAATTGGAGCAAGGA 1580
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Db 938 TCTGTGTGTGGTGGCCACATGGGTCTGTGGCAGGAGTCTTAATGTGAGGACAGAA 997
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QY 2061 CACACAGAACTTCTCAAGGCTACGACAGCATGTCACTGAAGAAACCTCACAAGCTGCG 2120
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QY 2121 CATGATAGCTGTGTCACTCTTGTAGTTCACCCGGGGGAA--TAGAGACTGGAAGCTTTC 2178
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Db 1535 CACGATGGCTGTGCTCTCTGTAGCCACCATATGAAAGCAAGAGACTTAAAGGCTTTC 1594
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QY 2179 TACTCTCCCTTCAGTGAACAATGCTGTGTGACGACTGTGA 2220
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Db 1595 TATTCACCAATTAACAGGAAACAAAGTGTGATGATCTGTA 1636
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RESULT 11
ABR03200
ID ABR03200 standard; cDNA; 1841 BP.
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AC ABA03200;
XX
XX 11-FEB-2002 (first entry)
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XX Human IL-17 receptor like protein #1 coding sequence.
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XX Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
XX antipsoriatic; antimicrobial; anorectic; neuroprotective;
XX antidiabetic; antiallergic; dermatological; cytostatic; gene therapy;
XX interleukin 17; immune system disorder; infection; weight; reproduction;
XX neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
XX glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
XX tumour; ss.
XX
XX Homo sapiens.
XX
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XX Key Location/Qualifiers
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XX FT /product="Human IL-17 receptor-like protein #1"
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XX 20-SEP-2001.
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XX 16-MAR-2001; 2001WO-US08688.
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XX PF 16-MAR-2000; 2000US-189923P.
XX PR 12-MAY-2000; 2000US-204208P.
XX PR 27-NOV-2000; 2000US-0723232.
XX PR 02-FEB-2001; 2001US-266159P.
XX
XX (AMGE-) AMGEN INC.
XX
XX PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ.
XX
XX WPI; 2002-055100/07.
XX DR P-PSDB; AAM47456.
XX
XX PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
XX PT polypeptides, useful for treating, diagnosing, ameliorating or
XX PT preventing immune system disorders (e.g. psoriatic arthritis) and
XX PT infections (e.g. viral infections).
XX
XX PS Claim 1; Fig 1; 239p; English.
XX
XX CC The present invention relates to novel human nucleic acids encoding
XX CC interleukin 17 (IL-17) receptor like proteins. The present sequence is
XX CC one such coding sequence. The IL-17 receptor-like proteins and coding
XX CC sequences are useful for treating a pathological condition related to
XX CC immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
XX CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction
XX CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
XX CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
XX CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.
XX CC ischaemia), eye disorders, reproductive disorders, tumours and
XX CC inflammation.
XX
XX SQ Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;
XX
XX
XX Query Match 24.8%; Score 643.2; DB 24; Length 1841;
XX Best Local Similarity 75.9%; Pred. No. 1.7e-181;
XX Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;
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XX QY 1113 TTACATTTCCAGGCTGCTTAACACGTAATATATTAAGACGTGCAAGGCG 1172
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Db 518 TTCACTCTCACAGGCTGCTTAACACCATTAATGAATATTAAGAAAGGTCTCAAGGCG 577
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QY 1173 GGAAGCCTGTGGAGCCACGACATCACTGCTTGTAAAGAAAGAGAGATGTTGAAGTG 1232
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Db 578 GGAAGCCTGTGGAGATTCAGACATCACTGCTTGTAAAGAAATGAGAGACAGTAAAGTG 637
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QY 1233 AATTTCACACCAATCCCTTGGAAAAGATACAGATTCCTATTCAACGGGACACGACA 1292
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[illegible]

RESULT 12
AAD28777
ID AAD28777 standard; DNA; 2015_BP
XX
AC AAD28777;

XX	07-MAY-2002	(first entry)
DT		
XX	Human Interleukin-17 receptor B-3 (IL-17RB-3) DNA.	
XX		
KW	Human, interleukin-17 receptor B-3; IL-17RB-3; immune system dysfunction,	
KW	Cytosarctic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;	
KW	Inflammatory bowel disease; neuronal dysfunction; transplant rejection;	
KW	autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;	
KW	infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;	
KW	cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;	
KW	eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;	
KW	leukemia; atherosclerosis; heart failure; angiogenesis; endometriosis;	
KW	lupus; retinal neuropathy; infertility; miscarriage; inflammation;	
KW	cancer; diabetes; ds.	
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OS	Homo sapiens.	
XX		
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FT	CDS	50..1732
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FT		/product= "Human IL-17RB-3 protein"
FT	sig_peptide	50..92
FT		/tag= b
FT	mat_peptide	93..1729
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FT		/product= "Mature IL-17RB-3 protein"
XX		
PN	WO200208285-A2.	
PD		
XX	31-JAN-2002.	
XX		
PR	21-JUN-2001; 2001WO-US19861.	
PR		
PR	22-JUN-2000; 2000US-213125P.	
PR	02-FEB-2001; 2001US-266159P.	
PR	16-MAR-2001; 2001US-0810384.	
PA	(AMGE-) AMGEN INC.	
PI		
PI	Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;	
DR	WPI; 2002-155217/20.	
DR	P-PDB; AAE18128.	
XX		
PT	Nucleic acid molecules encoding Interleukin 17 (IL-17) - like	
PT	polypeptides useful in the treatment, prevention and diagnosis of	
PT	diseases e.g. cancer -	
XX		
XX	Disclosure; Page 234-236; 242pp; English.	
PS		
XX	The invention relates to nucleic acid molecules encoding Interleukin 17	
CC	(IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels	
CC	of IL-17 protein in an animal. The IL-17 protein is useful for treating,	
CC	preventing or ameliorating a disease, such as immune system dysfunction	
CC	(rheumatoid arthritis, osteoarthritis, inflammatory joint disease);	
CC	autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel	
CC	disease, transplant rejection, graft vs. host disease); infections (HIV,	
CC	hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,	
CC	sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung	
CC	(acute respiratory distress syndrome, cystic fibrosis, emphysema); skin	
CC	(psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone	
CC	(osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy	
CC	atherosclerosis, heart failure, angiodysplasia); tumours, cancers (lymphoma	
CC	leukemia); reproductive (infertility, miscarriage, endometriosis); eye	
CC	(blindness, retinal neuropathy) and treatment of diseases involving	
CC	inflammation. The present sequence is human Interleukin-17 receptor B-3	
CC	(IL-17RB-3) DNA.	
XX		
SQ	Sequence 2015 BP; 541 A; 499 C; 475 G; 500 T; 0 other;	
XX		
Query Match	24.8%; Score 643.2; DB 24; Length 2015;	
Best Local Similarity	75.9%; Pred.No. 1.8e-181;	

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 XX AA52046;
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DT 09-AUG-2000 (first entry)
 XX cDNA encoding interleukin 17-like receptor protein (IL17RLP)-2.
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 KW Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
 KW resistant chronic infection; acute infection; mycobacterial infection;
 KW T-cell proliferation; IL-2 biosynthesis; lymphocytic leukemia;
 KW T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 KW IL-6 expression; myeloma; plasmacytoma; Lennert's lymphoma;
 KW immunoprotective; cytostatic; hematopoietic; proliferative;
 KW antibacterial; ss.
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 XX 23-MAR-2000.
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 XX 16-MAR-1999; 99US-0268311.
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 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Shi Y;
 XX
 XX MPI: 2000-271403/23.
 XX
 XX P-PSDB; AAT70595.
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 XX Novel polynucleotides encoding interleukin-17-like receptor protein,
 PT useful for diagnosis and treatment of immune system-related disorders,
 PT e.g. sepsis and cancers -
 XX
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 PS Disclosure, Page 141-143; 147pp; English.
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 XX The patent relates to novel interleukin-17-like receptor
 CC protein (IL-17RLP). IL-17RLP is a homologue of the IL-17 receptor and has
 CC a wide range of cytokine receptor-like activities. IL-17RLP or its
 CC agonists may be used to enhance host defenses against resistant chronic
 CC and acute infections, e.g. mycobacterial infections, via the attraction
 CC and activation of microbicidal leukocytes. It may also be used to
 CC increase T-cell proliferation by stimulating IL-2 biosynthesis, for the
 CC treatment of T-cell mediated autoimmune diseases and lymphocytic
 CC leukemias. IL-17RLP may also be used to regulate hematopoiesis and to
 CC treat sepsis. Extracellular IL-17RLP domains may be used as antagonists
 CC of IL-17RLP. IL-17RLP agonists and antagonists can also be used to
 CC modulate IL-6 expression, useful in treatment of cancers such as
 CC myelomas, plasmacytomas and hybridomas and Lennert's lymphoma. The
 CC present cDNA sequence encodes human IL-17RLP. This cDNA sequence was
 CC derived from sequencing the HAPOR40 cDNA clone (ATCC deposit
 CC number: 209198)
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TITLE Evi27 encodes a novel membrane protein with homology to the IL17 receptor

JOURNAL Oncogene 19 (17), 2098-2109 (2000)

MEDLINE 20273223

PUBMED 10815801

REFERENCE 2 (bases 1 to 2589)

AUTHORS Shaughnessy, J.D. Jr.

TITLE Direct Submission

JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W. Markham St, Little Rock, AR 72212, USA

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Source Location/Qualifiers

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 1 (bases 1 to 1963)
 Tian, E., Sawyer, J.R., Largespada, D.A., Jenkins, N.A., Copeland, N.G.
 and Shaughnessy, J.D., Jr.
 Evi27 encodes a novel membrane protein with homology to the IL17
 receptor
 JOURNAL Oncogene 19 (17), 2098-2109 (2000)
 MEDLINE 20273223
 PUBMED 10815801
 REFERENCE 2 (bases 1 to 1963)
 Shaughnessy, J.D., Jr.
 TITLE Direct Submission
 JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research
 Center, University of Arkansas for Medical Sciences, 4301 W.
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DEFINITION  IMAGE:5042466, mRNA, complete cds.
ACCESSION  BC026546
VERSION    BC026546.1  GI:20071644
KEYWORDS   MGC.

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SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2018)
TITLE	Strausberg, R.
JOURNAL	Direct Submission
COMMENT	Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
	Contact: MGC help desk
	Email: cgapdb-remail.nih.gov
	Tissue Procurement: Jeffrey E. Green, M.D.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULIN)
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
	Web site: http://www-sbpc.stanford.edu
	Contact: (Dickson, Mark) mcdgpaxil.stanford.edu
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES

Source

CDS

BASE COUNT ORIGIN	535 a	504 c	501 g	478 t
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Best Local Similarity	99.5%;	Pred. No. 0;		
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VERSION AX350967.1 GI:18616343
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ORGANISM unidentified.
REFERENCE 1
AUTHORS Gorman, D.M.
TITLE Mammalian receptor proteins; related reagents and methods
JOURNAL Patent: WO 0190358-A 1 29-NOV-2001;
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 AUTHORS Kato, S. and Kimura, T.
 TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
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 Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
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AUTHORS      Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
              Nguyen,H.Q.
TITLE        11-17 receptor like molecules and uses thereof
JOURNAL      Patent: WO 0168705-A 1 20-SEP-2001;
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VERSION AX365258.1 GI:18697003
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REFERENCE 1 Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S., Nguyen,H.Q. and
Jing,S.
TITLE 11-17 molecules and uses thereof
JOURNAL Patent: WO 0208285-A 17 31-JAN-2002;
Amgen, Inc. (US)
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 JING,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
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